

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 108 Seconds
(without alignments)
564.248 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKPKGASVKV.....YDYYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 48933398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

11: Geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	672	100.0	125	7	ADK18776	Adk18776	Anti-huma
2	672	100.0	125	7	ADK18948	Adk18948	Anti-huma
3	672	100.0	125	7	ADK18624	Adk18624	Anti-huma
4	672	100.0	125	7	ADK18813	Adk18813	Anti-huma
5	672	100.0	125	8	ADL25392	Human mAb	Adl25392
6	638	94.9	125	7	ADK18614	Adk18614	Anti-huma
7	638	94.9	125	7	ADK18779	Adk18779	Anti-huma
8	638	94.9	125	7	ADK18919	Adk18919	Anti-huma
9	638	94.9	125	7	ADK18816	Adk18816	Anti-huma
10	638	94.9	125	8	ADL25444	Human mAb	Adl25444
11	593.5	88.3	126	7	ADK18864	Adk18864	Anti-huma
12	593.5	88.3	126	7	ADK18595	Adk18595	Anti-huma
13	593.5	88.3	126	7	ADK18777	Adk18777	Anti-huma
14	593.5	88.3	126	8	ADL25408	Human mAb	Adl25408
15	598	87.5	123	10	AEK98538	Human ant	Aek98538
16	579.5	86.2	125	7	ADK18814	Adk18814	Anti-huma
17	578	86.0	119	10	AEH94456	Anti-ten-	Aeh94456
18	575.5	85.6	126	7	ADK18925	Adk18925	Anti-huma
19	575.5	85.6	126	7	ADK18780	Adk18780	Anti-huma
20	575.5	85.6	126	7	ADK18616	Adk18616	Anti-huma
21	575.5	85.6	126	7	ADK18817	Adk18817	Anti-huma
22	575.5	85.6	126	8	ADL25448	Human mAb	Adl25448

23	572	85.1	127	7	ADK18620	Adk18620 Anti-huma
24	572	85.1	127	7	ADK18818	Adk18818 Anti-huma
25	572	85.1	127	7	ADK18781	Adk18781 Anti-huma
26	572	85.1	127	7	ADK18936	Adk18936 Anti-huma
27	572	85.1	127	8	ADL25456	Adl25456 Human mAb
28	571	85.0	123	10	AEK98534	Aek98534 Human ant
29	570	84.8	126	10	AEI64964	Aei64964 Anti-Ang-
30	570	84.8	126	10	AEI64968	Aei64968 Anti-Ang-
31	567.5	84.4	126	7	ADK18597	Adk18597 Anti-huma
32	567.5	84.4	126	7	ADK18870	Adk18870 Anti-huma
33	567.5	84.4	126	7	ADK18812	Adk18812 Anti-huma
34	567.5	84.4	126	7	ADK18775	Adk18775 Anti-huma
35	567.5	84.4	126	8	ADL25412	Adl25412 Human mAb
36	566	84.2	127	10	AEJ20382	Aej20382 Anti-IRTA
37	564.5	84.0	124	10	AEI14838	Aei14838 Human ant
38	563.5	83.9	124	10	AEI14842	Aei14842 Human ant
39	561.5	83.6	122	6	ABR55829	Abr55829 Heavy cha
40	561.5	83.6	122	10	AEI17553	Aei17553 Human ang
41	561.5	83.6	126	7	ADK18778	Adk18778 Anti-huma
42	561.5	83.6	126	7	ADK18613	Adk18613 Anti-huma
43	561.5	83.6	126	7	ADK18815	Adk18815 Anti-huma
44	561.5	83.6	126	8	ADL25464	Adl25464 Human mAb
45	558.5	83.1	121	10	AEI65125	Aei65125 Anti-Ang-

ALIGNMENTS

RESULT 1

ADK18776

ID ADK18776 standard; protein; 125 AA.

AC ADK18776;

XX

DT 06-MAY-2004 (first entry)

XX

DE Anti-human PDGF-D antibody protein related sequence #2.

XX

KW antinflammatory; immunomodulator; cytostatic; gene therapy.

XX

OS Homo sapiens.

XX

PN WO2003057857-A2.

XX

PD 17-JUL-2003.

XX

PF 06-JAN-2003; 2003WO-US000398.

XX

PR 07-JAN-2002; 2002US-00041860.

XX

PA (ABGE-) ABGENIX INC..

XX

Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R; Bezabeh B;

XX

WPI; 2003-587119/55.

XX

PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

XX

PS Disclosure; SEQ ID NO 200; 255pp; English.

XX

CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX SQ Sequence 125 AA;
 Query Match 100.0%; Score 672; DB 7; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.4e-54;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 DB 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
 DB 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125
 DB 121 VTVSS 125

RESULT 2
 ADK18948
 ID ADK18948 standard; protein; 125 AA.
 AC ADK18948;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody protein related sequence #174.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057857-A2.
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 PT New human monoclonal antibody that binds to platelet-derived growth
 factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 372; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.

XX SQ Sequence 125 AA;
 Query Match 100.0%; Score 672; DB 7; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.4e-54;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

DB 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 QY 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
 DB 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125
 DB 121 VTVSS 125

RESULT 3
 ADK18624
 ID ADK18624 standard; protein; 125 AA.
 XX
 AC ADK18624;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody heavy chain protein sequence.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057857-A2.
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF; Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 PT New human monoclonal antibody that binds to platelet-derived growth
 factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 48; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.

XX SQ Sequence 125 AA;
 Query Match 100.0%; Score 672; DB 7; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.4e-54;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 DB 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
 DB 61 AQKFGQGRVTMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120

QY 121 VTVSS 125

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Db      121  VTVSS 125
|||||
RESULT 4
ADK18813
ID   ADK18813 standard; protein; 125 AA.
XX
AC   ADK18813;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #39.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
FI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 237; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 125 AA;

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
DB   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120

QY   121  VTVSS 125
DB   121  VTVSS 125

RESULT 5
ADL25392
ID   ADL25392 standard; protein; 125 AA.
XX
AC   ADL25392;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Human mab 6.4 heavy chain variable region protein SEQ ID NO:2.
XX
KW   antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW   nephritis; mesangial cell proliferation inhibition;
KW   mesangial proliferative glomerulonephritis; nephrotropic;
KW   antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW   gene therapy; human; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
PN   WO2004024098-A2.
XX
PD   25-MAR-2004.
XX
PF   16-SEP-2003; 2003WO-US029414.
XX
PR   16-SEP-2002; 2002US-0411137P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (CURA-) CURAGEN CORP.
XX
PI   Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
DR   WPI; 2004-269881/25.
DR   N-PSDB; ADL25391.
XX
PT   Use of an antibody or its binding fragment that binds platelet derived
PT   growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT   nephritis.
XX
PS   Disclosure; SEQ ID NO 2; 115pp; English.
XX
CC   The present invention describes an antibody or its binding fragment that
CC   binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC   useful in preparing a medicament for treating nephritis. Also described:
CC   (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC   (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC   of treating mesangial proliferative glomerulonephritis. The antibody has
CC   nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC   antidiabetic activities, and can be used in gene therapy. The antibody or
CC   its binding fragment, that binds PDGF-DD, can be used in preparing a
CC   medicament for treating nephritis and related disorders, e.g., mesangial
CC   proliferative glomerulonephritis. The present sequence represents a human
CC   monoclonal antibody (mAb) variable region sequence, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 125 AA;

Query Match      100.0%; Score 672; DB 8; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

QY   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
DB   61 AQKFGQVRVTMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120

QY   121  VTVSS 125
DB   121  VTVSS 125

RESULT 6
ADK18614
ID   ADK18614 standard; protein; 125 AA.
XX

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PR 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 343; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX
XX Sequence 125 AA;
XX
XX Query Match 94.9%; Score 638; DB 7; Length 125;
XX Best Local Similarity 94.4%; Pred. No. 4.7e-51;
XX Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 QVOLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNSGNTDY 60
DB 1 QVOLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNSGNTGY 60
QY 61 AQKFGQRTVMTRTDTSISTAYMELSSLRSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQRTVMTRTDTSISTAYMELSSLRSEDTAVVYCARGSGSYGYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125
RESULT 10
ADL25444
ID ADL25444 standard; protein; 125 AA.
XX
XX ADL25444;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human mAb 1.45 heavy chain variable region protein SEQ ID NO:54.
XX
XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
XX nephritis; mesangial cell proliferation inhibition;
XX mesangial proliferative glomerulonephritis; nephrotropic;
XX antinflammatory; dermatological; immunosuppressive; antidiabetic;
XX gene therapy; human; monoclonal antibody; mAb.
XX
XX Homo sapiens.
XX
XX WO2004024098-A2.
XX
XX 25-MAR-2004.
XX
XX 16-SEP-2003; 2003WO-US029414.
XX
XX 16-SEP-2002; 2002US-0411137P.
XX
XX (ABGE-) ABGENIX INC.
XX (CURA-) CURAGEN CORP.
XX
XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
XX WPI; 2004-269881/25.
XX N-PSDB; ADL25443.
XX
XX Use of an antibody or its binding fragment that binds platelet derived
XX growth factor-DD (PDGF-DD) for preparing a medicament for treating

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PT nephritis.
 PS Disclosure; SEQ ID NO 54; 115pp; English.
 XX
 CC The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and CC antidiabetic activities, and can be used in gene therapy. The antibody or CC its binding fragment, that binds PDGF-DD, can be used in preparing a CC medicament for treating nephritis and related disorders, e.g., mesangial CC proliferative glomerulonephritis. The present sequence represents a human CC monoclonal antibody (mAb) variable region sequence, which is used in the CC exemplification of the present invention.
 XX
 SQ Sequence 125 AA;
 Query Match 94.9%; Score 638; DB 8; Length 125;
 Best Local Similarity 94.4%; Pred. No. 4.7e-51;
 Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTDY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTGY 60
 QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
 DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
 QY 121 VTSS 125
 DB 121 VTSS 125
 RESULT 11
 ADK18864
 ID ADK18864 standard; protein; 126 AA.
 AC ADK18864;
 DT 06-MAY-2004 (first entry)
 XX Anti-human PDGF-D antibody protein related sequence #90.
 DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
 KW Homo sapiens.
 OS
 XX WO2003057857-A2.
 FN 17-JUL-2003.
 XX
 XX 06-JAN-2003; 2003WO-US000398.
 XX
 XX 07-JAN-2002; 2002US-00041860.
 PR (ABGE-) ABGENIX INC.
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 PA (ABGE-) ABGENIX INC.
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 PS Disclosure; SEQ ID NO 288; 255pp; English.
 XX The invention relates to a human monoclonal antibody that binds to
 CC

CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.
 XX
 SQ Sequence 126 AA;
 Query Match 88.3%; Score 593.5; DB 7; Length 126;
 Best Local Similarity 89.7%; Pred. No. 6.1e-47;
 Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
 QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTDY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTGY 60
 QY 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
 DB 61 AQKFGQRTVMTTRDTSISTAYMELSLRSEDTAIYYCAREGIAVAGTYYYGMDVWGQGT 120
 QY 120 TVTSS 125
 DB 121 TVTSS 126
 RESULT 12
 ADK18595
 ID ADK18595 standard; protein; 126 AA.
 AC ADK18595;
 DT 06-MAY-2004 (first entry)
 XX Anti-human PDGF-D antibody heavy chain protein sequence.
 DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
 KW Homo sapiens.
 OS
 XX WO2003057857-A2.
 FN 17-JUL-2003.
 XX
 XX 06-JAN-2003; 2003WO-US000398.
 XX
 XX 07-JAN-2002; 2002US-00041860.
 PR (ABGE-) ABGENIX INC.
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR New human monoclonal antibody that binds to platelet-derived growth
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human
 PT diseases, such as inflammation, autoimmunity and cancer.
 PA (ABGE-) ABGENIX INC.
 XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

CC sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 6.1e-47;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGVMTTRTSTISITAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYGGMDVWGQGT 119

DB 61 AQKFGQGVMTTRTSTISITAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGGMDVWGQGT 120

QY 120 TTVTVSS 125

DB 121 TTVTVSS 126

RESULT 13

ADK18777
ID ADK18777 standard; protein; 126 AA.

AC ADK18777;

XX 06-MAY-2004 (first entry)

DT 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody protein related sequence #3.

DE antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX Homo sapiens.

OS WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;

PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth

PT factor-D (PDGF-D), useful for treating chronic and recurrent human

XX diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 201; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to

CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for

CC treating chronic and recurrent human diseases, such as inflammation,

CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are

CC useful for modulating collagen formation, and for staging various

CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were

CC generated using an active protein fragment of the gene product from the

CC clone 30664188.0.99 arising in the conditioned medium obtained when

CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

CC sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 88.3%; Score 593.5; DB 7; Length 126;

Best Local Similarity 89.7%; Pred. No. 6.1e-47;

Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGVMTTRTSTISITAYMELSSLRSEDTAIYYCVR-GFGYSYNYDYGGMDVWGQGT 119

DB 61 AQKFGQGVMTTRTSTISITAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGGMDVWGQGT 120

QY 120 TTVTVSS 125

DB 121 TTVTVSS 126

RESULT 14

ADL25408
ID ADL25408 standard; protein; 126 AA.

AC ADL25408;

XX 17-JUN-2004 (first entry)

DT 17-JUN-2004 (first entry)

XX Human mAb 1.18 heavy chain variable region protein SEQ ID NO:18.

DE antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;

XX nephritis; mesangial cell proliferation inhibition;

KW mesangial proliferative glomerulonephritis; nephrotropic;

KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;

KW gene therapy; human; monoclonal antibody; mAb.

XX Homo sapiens.

OS WO2004024098-A2.

XX 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.

XX (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;

XX WPI; 2004-269881/25.

XX N-PSDB; ADL25407.

XX Use of an antibody or its binding fragment that binds platelet derived

PT growth factor-DD (PDGF-DD) for preparing a medicament for treating

XX nephritis.

XX Disclosure; SEQ ID NO 18; 115pp; English.

XX The present invention describes an antibody or its binding fragment that

CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is

CC useful in preparing a medicament for treating nephritis. Also described:

CC (1) a method of detecting nephritis; (2) a method of treating nephritis;

CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method

CC of treating mesangial proliferative glomerulonephritis. The antibody has

CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and

CC antidiabetic activities, and can be used in gene therapy. The antibody or

CC its binding fragment, that binds PDGF-DD, can be used in preparing a

CC medicament for treating nephritis and related disorders, e.g., mesangial

CC proliferative glomerulonephritis. The present sequence represents a human

CC monoclonal antibody (mAb) variable region sequence, which is used in the

CC exemplification of the present invention.

XX Sequence 126 AA;

Query Match 88.3%; Score 593.5; DB 8; Length 126;

Best Local Similarity 89.7%; Pred. No. 6.1e-47;

Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AOKFQGRVTMTTRDTSISTAYMELSSLRSBEDTAIYYCVRFSGYSYNYDYYYGMDVWGQGT 119
Db 61 AOKFQGRVTMTTRNTSISTAYMELSSLRSBEDTAIYYCAREGIAVAGTYYYYYYGMVWGQGT 120
QY 120 TVTVSS 125
Db 121 TVTVSS 126
RESULT 15
AEK98538
ID AEK98538 standard; protein; 123 AA.
XX AC AEK98538;
XX DT 30-NOV-2006 (first entry)
XX DE Human anti-Ten-M2 antibody heavy chain variable region, SEQ ID:50.
XX KW monoclonal antibody; antibody therapy; Ten-M2; diagnosis; pharmaceutical;
XX KW tumor; cytostatic; neoplasm; cancer; heavy chain variable region.
XX OS Homo sapiens.
XX PN WO2006104978-A2.
XX PD 05-OCT-2006.
XX PF 27-MAR-2006; 2006WO-US011031.
XX PR 25-MAR-2005; 2005US-0665592P.
XX PA (CURA-) CURAGEN CORP.
XX PA (ABGE-) ABGENIX INC.
XX PI Ettenberg S, Masterman S, Larochele W, Zhong H;
XX WPI; 2006-670467/69.
XX DR
XX PT New fully human monoclonal antibody that binds to Ten-M2 and neutralizes
XX PT Ten-M2 activity, useful for treating symptoms and conditions associated
XX PT with Ten-M2 activity, e.g. cancer.
XX PS Claim 5; SEQ ID NO 50; 141pp; English.
XX CC The new invention relates to a fully human monoclonal antibody or its
XX CC binding fragment that binds to Ten-M2 and neutralizes Ten-M2 activity.
XX CC Also described are a method for assaying the level of Ten-M2 in a patient
XX CC sample; a composition comprising the antibody or its binding fragment and
XX CC a pharmaceutical carrier; and a method of treating malignant tumors. The
XX CC antibody is a full-length antibody. Alternatively, the human monoclonal
XX CC antibody that binds to Ten-M2 comprises a heavy chain having an amino
XX CC acid sequence selected from any of fully defined 116-127 amino acid
XX CC sequences (SEQ ID NO. 2, 6, 10, 14, 18, 22, 26, 30, 34, 38, 42, 46, or
XX CC 50) given in the specification. It also comprises a light chain having an
XX CC amino acid sequence selected from any of fully defined 101-113 amino acid
XX CC sequences (SEQ ID NO. 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, or
XX CC 52) given in the specification. Alternatively, the antibody or its
XX CC binding fragment binds to Ten-M2, where the antibody or binding fragment
XX CC neutralizes a Ten-M2-induced activity, and where the antibody or binding
XX CC fragment cross-reacts with a fully human anti-Ten-M2 antibody selected
XX CC from Mab120, Mab140, and Mab171, Mab179, Mab199, Mab213, or an antibody
XX CC in the same antigen-binding bin as fully human anti-Ten-M2 antibody
XX CC Mab120, Mab140, and Mab171, Mab179, Mab199, or Mab213. Assaying the level
XX CC of Ten-M2 in a patient sample comprises contacting the patient sample
XX CC with the anti-Ten-M2 antibody, and determining the presence or amount of
XX CC anti-Ten-M2 antibody bound to Ten-M2, thus detecting the level of Ten-M2
XX CC in the patient sample. The antibodies can be used for treating symptoms
XX CC and conditions associated with Ten-M2 activity, e.g. cancer. This

CC sequence is a human anti-Ten-M2 antibody heavy chain variable region
CC protein sequence.
XX
SQ Sequence 123 AA;
Query Match 87.5%; Score 588; DB 10; Length 123;
Best Local Similarity 89.6%; Pred. NO. 1.9e-46;
Matches 112; Conservative 5; Mismatches 6; Indels 2; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60
QY 61 AOKFQGRVTMTTRDTSISTAYMELSSLRSBEDTAIYYCVRFSGYSYNYDYYYGMDVWGQGT 120
Db 61 AOKFQGRVTMTTRNTSISTAYMELSSLRSBEDTAIYYCARGPGGSFY--YYGMDVWGQGT 118
QY 121 TVTVSS 125
Db 119 TVTVSS 123

Search completed: April 25, 2007, 04:05:20
Job time : 109.404 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 10 Seconds
(without alignments)
1261.509 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQVQSGAEVKKPGASVKV.....YDYVGMVWGQTTVTSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	82.9	127	2 S34014	Ig heavy chain V r
2	537.5	80.0	136	2 S31600	Ig heavy chain V r
3	534	79.5	129	2 S46393	Ig heavy chain V r
4	516.5	76.9	118	2 S36265	Ig heavy chain V r
5	515	76.6	123	2 S33548	Ig heavy chain V-1
6	514	76.5	129	2 S36260	Ig heavy chain V r
7	511.5	76.1	135	2 S49530	anti-Sm antibody V
8	510.5	76.0	132	2 S31596	Ig heavy chain V r
9	500	74.4	131	2 S26792	Ig heavy chain V r
10	499	74.3	119	2 PH0961	Ig heavy chain V r
11	496.5	73.9	110	2 PH1670	Ig heavy chain V r
12	496	73.8	98	2 S26918	Ig heavy chain V r
13	495.5	73.7	132	2 PH0954	Ig heavy chain V r
14	495.5	73.7	171	2 S23623	Ig heavy chain V r
15	494.5	73.6	118	2 PH1666	Ig heavy chain V r
16	493.5	73.4	136	2 PH0960	Ig heavy chain V r
17	488.5	72.7	143	1 E1HUND	Ig heavy chain pre
18	488	72.6	127	2 PH0955	Ig heavy chain V r
19	487.5	72.5	124	2 S19665	Ig heavy chain V r
20	486	72.3	133	2 C33548	Ig heavy chain V-1
21	486	72.3	627	2 S14683	Ig mu chain precu
22	484	72.0	142	2 A32483	Ig heavy chain V r
23	480	71.4	122	2 S36271	Ig heavy chain V r
24	480	71.4	160	2 PLO105	anti-PR2 erythrocy
25	477.5	71.1	126	2 S33548	Ig heavy chain V-1
26	476.5	70.9	114	2 PH1667	Ig heavy chain V r
27	473.5	70.5	128	2 PH0952	Ig heavy chain V r
28	472.5	70.3	120	2 S31999	Ig heavy chain V r
29	468	69.6	109	2 PH1668	Ig heavy chain V r

```

30 465 69.2 98 2 S26938 Ig heavy chain V r
31 465 69.2 117 2 S31680 Ig heavy chain V r
32 465 69.2 117 2 S18551 Ig heavy chain V r
33 465 69.2 126 2 I44151 Ig heavy chain V r
34 463 68.9 104 2 S69899 Ig heavy chain V r
35 462 68.8 121 2 S20783 Ig heavy chain V r
36 460.5 68.5 122 2 PH0958 Ig heavy chain V r
37 457 68.0 98 2 S26912 Ig heavy chain V r
38 456 67.9 125 2 PH0957 Ig heavy chain V r
39 455.5 67.8 120 2 S26789 Ig heavy chain V r
40 454.5 67.6 132 2 S46394 Ig heavy chain V r
41 454 67.6 129 2 A33548 Ig heavy chain V-1
42 452.5 67.3 110 2 PH1669 Ig heavy chain V r
43 449 66.8 125 2 S68170 Ig heavy chain V r
44 448.5 66.7 116 2 PH0959 Ig heavy chain V r
45 446.5 66.4 135 2 B32274 Ig heavy chain pre

```

ALIGNMENTS

RESULT 1

S34014

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C;Accession: S34014; S30535

R;Marette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A;Reference number: S34001; MUID:93209281; PMID:7681398

A;Accession: S34014

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-127 <VAR>

A;Cross-references: UNIPARC:UPI0000176D31; EMBL:Z18321

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 557; DB 2; Length 127;

Best Local Similarity 82.7%; Pred. No. 1.4e-42;

Matches 105; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

```

Qy 1 QVQLVQSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTDY 60
Db 1 QVQVQSGAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWNPNSGNTGY 60
Qy 61 AQKFGKRVMTTRDTSTSTAYMELSSLESDTAIYCVR--GFGYSYNYDYVGMVWGQ 118
Db 61 AQKFGKRVMTTRDTSTSTAYMELSSLESDTAIYCVR--GFGYSYNYDYVGMVWGQ 118
Qy 119 TTVTVSS 125
Db 121 TTVSVSS 127

```

RESULT 2

S31600

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31600

R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31600

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <CUI>

A;Cross-references: UNIPARC:UPI0000116453; EMBL:Z14165; NID:q30994; PIDN:CAA78534.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
 S36260
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C:Accession: S36260
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBL J. 12, 725-734, 1993
 A:Title: Human anti-self antibodies with high specificity from phage display library
 A:Reference number: S36256; MUID:93178448; PMID:7679990
 A:Accession: S36260
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <GI>
 A:Cross-references: UNIPARC:UPI0000118DEB; EMBL:Z18851; NID:G33124; PIDN:CAA79393
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 514; DB 2; Length 129;
Best Local Similarity 78.3%; Pred. No. 9.3e-39;
Matches 101; Conservative 8; Mismatches 16; Indels 4; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWISAYNGNTNY 60
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYCVRG-FGFSYNYD---YYGMDVWG 116
DB 61 AQKLGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYCVRG-FGFSYNYD---YYGMDVWG 120
QY 117 QGTTVTVSS 125
DB 121 KGTITVSS 129

RESULT 7
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
R:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAP>
A:Cross-references: UNIPARC:UPI00001166FF; EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID: F:34-117/Domain: immunoglobulin V region; immunoglobulin homology <IMM>

Query Match 76.1%; Score 511.5; DB 2; Length 135;
Best Local Similarity 79.4%; Pred. No. 1.6e-38;
Matches 100; Conservative 6; Mismatches 9; Indels 11; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPQGLEWGWINPNSGGTNY 79
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYCVRG-FGFSYNYDYYGMDVWGQGT 119
DB 80 AQKFGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYCVRG-FGFSYNYDYYGMDVWGQGT 129
QY 120 TVTVSS 125
DB 130 LVTSS 135

RESULT 8
S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R:Accession: S31596
R:Cuinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31596
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: UNIPARC:UPI0000116454; EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID: F:34-117/Domain: immunoglobulin V region; immunoglobulin homology
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 510.5; DB 2; Length 132;

Best Local Similarity 79.2%; Pred. No. 1.9e-38;
Matches 99; Conservative 6; Mismatches 7; Indels 13; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTGY 79
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYCVRGFGFSYNYDYYGMDVWGQGT 120
DB 80 AQKFGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYLAKA-----PAWGQGT 126
QY 121 TVTVSS 125
DB 127 TVTVSS 131

RESULT 9
S26792
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26792
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family.
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26792
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <MOR>
A:Cross-references: UNIPARC:UPI0000115FC3; EMBL:X61012; NID:G32804; PIDN:CAA43346.1; PID: F:15-98/Domain: immunoglobulin V region; immunoglobulin homology
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 500; DB 2; Length 131;
Best Local Similarity 72.5%; Pred. No. 1.6e-37;
Matches 95; Conservative 13; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMNVRQAPQGLEWGWINTGNTPT 60
QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSY-----NYDYVYGMV 114
DB 61 AQKFGQGRVTMTSDTSISTAYLQISLKAEDTAIYYCARDGRGYSYDFWGSFYFYTYMDV 120
QY 115 WGQGTITVSS 125
DB 121 WGQGTITVSS 131

RESULT 10
PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0961
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <MAP>
A:Cross-references: UNIPARC:UPI0000176CE5
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2

Query Match 73.7%; Score 495.5; DB 2; Length 171;
 Best Local Similarity 70.9%; Pred. No. 5.5e-37;
 Matches 95; Conservative 9; Mismatches 13; Indels 17; Gaps 2;

QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 20 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 79
 QY 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYG----- 111
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 80 GQKFGQRTVMTSDTSISTAYMELSLRSDTAVYYCA-----IEFYDGSDLKPSDV 131

QY 112 MDVWGQGTITVTVSS 125
 Db :|||||:|||||
 132 FDIWGQGTITVTVSS 145

RESULT 15
 PHI666
 Ig heavy chain V region (clone 6C9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PHI666
 R: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
 A:Reference number: PHI642; MUID:93301610; PMID:8315388
 A:Accession: PHI666
 A:Molecule type: mRNA
 A:Residues: 1-118 <HIL>
 A:Cross-references: UNIPARC:UPI0000176BE7
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F; 7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 494.5; DB 2; Length 118;
 Best Local Similarity 80.5%; Pred. No. 4.5e-37;
 Matches 95; Conservative 6; Mismatches 16; Indels 1; Gaps 1;

QY 9 AEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQKFGQGRV 68
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 AEVKPKGASVKSCASGYTFTSYAMHWVRQAPGQRLWGMWINAGNGNTKYAQKFGQGRV 60

QY 69 TMTSDTSISTAYMELSLRSEDTAIYVCVR-GFGYSYNDYYGMDVWGQGTITVTVSS 125
 Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 61 TITSDTSISTAYMELSLRSEDTAIYVCARVTLGGIKIFYYGYGMDVWGQGTITVTVSS 118

Search completed: April 25, 2007, 04:06:39
 Job time : 9.5339 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 85 Seconds
(without alignments)
1574.822 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 8.4.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	497.5	74.0	159	2	Q96QSO HUMAN	Q96QSO homo sapien
2	494	73.5	119	2	Q9UL94 HUMAN	Q9UL94 homo sapien
3	494	73.5	125	2	Q9UL95 HUMAN	Q9UL95 homo sapien
4	491	73.1	244	2	Q6SZC8 HUMAN	Q6SZC8 homo sapien
5	488.5	72.7	147	1	HVIC HUMAN	P01744 homo sapien
6	481.5	71.7	124	2	Q9UL92 HUMAN	Q9UL92 homo sapien
7	478.5	71.2	498	2	Q6N041 HUMAN	Q6N041 homo sapien
8	474	70.5	497	2	Q8FY24 HUMAN	Q8FY24 homo sapien
9	470.5	70.0	500	2	Q8BRV0 HUMAN	Q8BRV0 homo sapien
10	457.5	68.1	518	2	Q6N030 HUMAN	Q6N030 homo sapien
11	455	67.7	119	2	Q9GYZ2 MOUSE	Q9GYZ2 mus musculus
12	446	66.4	500	2	Q6N091 HUMAN	Q6N091 homo sapien
13	441	65.6	117	1	HVIC HUMAN	P23083 homo sapien
14	440	65.5	117	1	HVIC HUMAN	P01743 homo sapien
15	438	65.2	480	2	Q6P089 HUMAN	Q6P089 homo sapien
16	436	64.9	458	2	Q5BJZ2 RAT	Q5BJZ2 mus musculus
17	433.5	64.5	469	2	Q7Z7P5 MOUSE	Q7Z7P5 mus musculus
18	430	64.0	481	2	Q9LW11 MOUSE	Q9LW11 mus musculus
19	429.5	63.9	116	2	Q9UL89 HUMAN	Q9UL89 homo sapien
20	425.5	63.3	145	2	Q924R4 MOUSE	Q924R4 mus musculus
21	425	63.2	519	2	Q5BBM2 HUMAN	Q5BBM2 homo sapien
22	424.5	63.2	617	2	Q4KML5 MOUSE	Q4KML5 mus musculus
23	422	62.8	147	2	Q925S3 MOUSE	Q925S3 mus musculus
24	420	62.5	157	2	Q95978 HUMAN	Q95978 homo sapien
25	419.5	62.4	475	2	Q6N095 HUMAN	Q6N095 homo sapien
26	419	62.4	470	2	Q7TMK1 MOUSE	Q7TMK1 mus musculus
27	418.5	62.3	118	1	HV51 MOUSE	P06330 mus musculus
28	418	62.2	117	2	Q9QXE9 MOUSE	Q9QXE9 mus musculus
29	417	62.1	472	2	Q6PJA7 MOUSE	Q6PJA7 mus musculus
30	417	62.1	473	2	Q9DBL4 MOUSE	Q9DBL4 mus musculus
31	416.5	62.0	463	2	Q99LC4 MOUSE	Q99LC4 mus musculus

32	415.5	61.8	145	2	Q924Q6 MOUSE	Q924Q6 mus musculus
33	414	61.6	117	1	HV12 MOUSE	P01756 mus musculus
34	414	61.6	146	2	Q924Q3 MOUSE	Q924Q3 mus musculus
35	413.5	61.5	145	2	Q924R1 MOUSE	Q924R1 mus musculus
36	413	61.5	120	1	HV03 MOUSE	P01747 mus musculus
37	413	61.5	468	2	Q569F9 MOUSE	Q569F9 mus musculus
38	412.5	61.4	143	2	Q924Q5 MOUSE	Q924Q5 mus musculus
39	412.5	61.4	145	2	Q924R3 MOUSE	Q924R3 mus musculus
40	412.5	61.4	134	2	Q8VCX7 MOUSE	Q8VCX7 mus musculus
41	412	61.3	134	2	Q652R6 MOUSE	Q652R6 mus musculus
42	410.5	61.1	145	2	Q924Q9 MOUSE	Q924Q9 mus musculus
43	410	61.0	598	2	Q568Y0 RAT	Q568Y0 rattus norv
44	409.5	60.9	143	2	Q924R0 MOUSE	Q924R0 mus musculus
45	409.5	60.9	465	2	Q6PJB2 MOUSE	Q6PJB2 mus musculus

ALIGNMENTS

RESULT 1
Q96QSO_HUMAN PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001, integrated into UniProtKB/TREMBL.
DT 01-DEC-2001, sequence version 1.
DT 18-APR-2006, entry version 21.
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY039025; AAK82649.1; -; mRNA.
DR HSSP; P01869; 1AE6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;

Query Match 74.0%; Score 497.5; DB 2; Length 159;

Best Local Similarity 74.0%; Pred. No. 1e-41;

Matches 97; Conservative 12; Mismatches 15; Indels 7; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNSGNTDY 60

Db 20 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQAPGQGPWMGVINPSSGARY 79

QY 61 AKFGQRTWTRDTSTSTAYMELSSLRSEDTAIYCVR-----GFQSYNYDYIGMDV 114

Db 80 SKQFQRLTWTRDTSTSTAYMELSSLRSEDTAIYCVR-----GFQSYNYDYIGMDV 138

QY 115 WGQGTITVTVSS 125

Db 139 WGQGTITVTVSS 149

RESULT 2

Q9UL94_HUMAN

ID Q9UL94_HUMAN PRELIMINARY; PRT; 119 AA.

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AC Q9UL94;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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DR EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INOB.
DR SMR; Q9UL94; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
FT NON_TER 119
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13B64F5345F4A16E CRC64;

Query Match 73.5%; Score 494; DB 2; Length 119;
Best Local Similarity 76.0%; Pred. No. 1.7e-41;
Matches 95; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 EVQLVESGAEVKPGASVKVSCKASGYTFTGYMHWRQAPCGGLEWGMWNPNSWTNI 60
QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 AQKFGQGVMTKDTSTISAYMELSLRSDTAIYCVARGGLWF-----DPWGQGT 114

QY 121 VTVSS 125
Db :||||
115 VTVSS 119

RESULT 3
Q9UL95 HUMAN
ID Q9UL95 HUMAN PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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-----
DR EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INOB.
DR SMR; Q9UL95; 1-122.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 125
FT NON_TER 125
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 73.5%; Score 494; DB 2; Length 125;
Best Local Similarity 76.0%; Pred. No. 1.8e-41;
Matches 95; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTDY 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 EVQLVESGAEVKPGASVKVSCKASGYTFTGYMHWRQAPCGGLEWGMWNPNSGNTNY 60
QY 61 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 AQKFGQGVMTTRDTSISTAYMELSLRSDTAIYCVARGGLWF-----DPWGQGT 114

QY 121 VTVSS 125
Db :||||
121 VTVSS 125

RESULT 4
Q65ZC8 HUMAN
ID Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 10.
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
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DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.

```

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KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 73.1%; Score 491; DB 2; Length 244;
Best Local Similarity 75.4%; Pred. No. 7.5e-41;
Matches 95; Conservative 13; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AQKFGQVRVMTTRDTSISTAYMELSSLRSEDTAIYICVR-GFGYSVNYDYIYGMVWGQGT 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AQKFGQVRVMTTRDTSISAAVMEVSLRSDDTAVYICAREGTGSA-----IYGMVWGQGT 115

QY 120 TVTVSS 125
   |||||
Db 116 LVTVSS 121

RESULT 5
HVIC_HUMAN STANDARD; PRT; 147 AA.
ID HVIC_HUMAN PRELIMINARY; PRT; 124 AA.
AC P01744;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 30-MAY-2006, entry version 47.
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molsgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP PROTEIN SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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CC
CC HSSP; P01751; INQB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain;
KW Direct protein sequencing; Immunoglobulin acid; Signal.
FT SIGNAL 1
FT CHAIN 20 147 Ig heavy chain V-I region ND.
FT MOD_RES 20 131 /FTid=PRO_0000015246.
FT FT 20 20 Ig-like.
FT FT 20 20 Pyrrolidone carboxylic acid.
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QY 61 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVRGFGSYNDYVYGGMDVWGQGT 120
DB 61 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVRGFGSYNDYVYGGMDVWGQGT 119
QY 121 VTVSS 125
DB 120 VTVSS 124

RESULT 7
QGN041 HUMAN PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE Hypothetical protein DKFZp686O16217 (Fragment).
GN Name=DKFZp686O16217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BX640710; CAE45829.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6N041; 268-476.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1-set.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON TR 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 71.2%; Score 478.5; DB 2; Length 498;
Best Local Similarity 74.6%; Pred. No. 3.1e-39;
Matches 94; Conservative 11; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASQYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 35 QVQLVQSGADVKKPGASVKVSCKASQYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 94
QY 61 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 119
DB 95 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 152
QY 120 VTVSS 125
DB 153 LVTSS 158

RESULT 8
QGN041 HUMAN PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE Hypothetical protein DKFZp686O16217 (Fragment).
GN Name=DKFZp686O16217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BX640710; CAE45829.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6N041; 268-476.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1-set.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON TR 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;

Query Match 71.2%; Score 478.5; DB 2; Length 498;
Best Local Similarity 74.6%; Pred. No. 3.1e-39;
Matches 94; Conservative 11; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASQYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 35 QVQLVQSGADVKKPGASVKVSCKASQYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 94
QY 61 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 119
DB 95 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVR- - - - -GFGYSYNDYVYGGMDVWGQGT 152
QY 120 VTVSS 125
DB 153 LVTSS 158

RESULT 9
QGN041 HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6N041;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 25-JUL-2006, entry version 36.
DE IGHA1 protein.
GN Name=IGHA1;
OS Homo sapiens (Human).

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Q8WY24_HUMAN
ID Q8WY24_HUMAN PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 27-JUN-2006, entry version 25.
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF283666; AAL36987.1; -; mRNA.
DR HSSP; P01876; 1OW0.
DR SMR; Q8WY24; 267-475.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019883; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1-set.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 497 AA; 53666 MW; F24D08DFAS663E5 CRC64;

Query Match 70.5%; Score 474; DB 2; Length 497;
Best Local Similarity 70.0%; Pred. No. 8.6e-39;
Matches 91; Conservative 13; Mismatches 16; Indels 10; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASQYFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 20 QEQLEQSGAEVTKPGASVKVSCKASQYFTSYDINWVRQAPGQGLEWMGMNPTGNTGF 79
QY 61 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVR- - - - -GFGYSYNDYVYGGMDVW 115
DB 80 AQLFQGRVTMTDTSISTAYMELSLRSEDIAIYCVR- - - - -GFGYSYNDYVYGGMDVW 134
QY 116 GQGTTVTVSS 125
DB 135 GHGTLVTVSS 144

RESULT 9
Q8WY24_HUMAN PRELIMINARY; PRT; 500 AA.
AC Q8WY24;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 25-JUL-2006, entry version 36.
DE IGHA1 protein.
GN Name=IGHA1;
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RG Mammalian Gene Collection Program Team;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RG NIH MGC Project;
RG Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; BC005951; AAH05951.1; -; mRNA.
DR HSP; P01876; IOW0.
DR SMR; Q9BRV0; 25-300, 270-478.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR013151; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 70.0%; Score 470.5; DB 2; Length 500;
Best Local Similarity 71.9%; Pred. No. 2e-38;
Matches 92; Conservative 11; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGCGLEWVGWGINPNSGNTDY 60
DB 20 QVHLVQSGAEVMPGASVRSVCKTSYGFHTSYIIWVRQAPGQGLEWVGWISPSDNTFR 79
QY 61 AQKFGQGRVTMTDTSISTAYMELSSLRSEDATLYYCVRGF-GYS---YNYDYGGMDVWGQ 117

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QY      121 VTVSS 125
DB      137 VTVSS 141
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RESULT 11
Q9GY22 MOUSE PRELIMINARY; PRT; 119 AA.
AC Q9GY22
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: AF282622; AAG01452.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q9GY22; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA993873FD5FA6AB CRC64;

Query Match 67.7%; Score 455; DB 2; Length 119;
Best Local Similarity 69.6%; Pred. No. 1.4e-37;
Matches 87; Conservative 14; Mismatches 18; Indels 6; Gaps 1;

QY      1 QVQLVQSGAEVKPKGASVKVSCASGYTFTSYDINNVRQATQGLQGLWGMGWINPNSGNTDY 60
DB      1 QVQLVESGAEVKPKGASVKVSCASGYTFTGYMNVVRQAPGHGLEWIGYINPSRGYTNV 60
|||||
QY      61 AQKFGRTVMTDTSISTAYMELSLRSEDTRAIYCVRGFGYSYNDYYGMDVVGQGT 120
DB      61 NQKFRDRTVMTDTSFKSTAYMDLSRLSADSAAVYVCAR-----YYDHYCLDYVGQGT 114
|||||
QY      121 VTVSS 125
DB      115 VTVSS 119
|||||
RESULT 12
Q6N091 HUMAN PRELIMINARY; PRT; 500 AA.
AC Q6N091;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 18-APR-2006, entry version 13.
DE Hypothetical protein DKFP686C02220 (Fragment).
GN Name=DKFP686C02220;

Query Match 67.7%; Score 455; DB 2; Length 119;
Best Local Similarity 69.6%; Pred. No. 1.4e-37;
Matches 87; Conservative 14; Mismatches 18; Indels 6; Gaps 1;

QY      1 QVQLVQSGAEVKPKGASVKVSCASGYTFTSYDINNVRQATQGLQGLWGMGWINPNSGNTDY 60
DB      1 QVQLVESGAEVKPKGASVKVSCASGYTFTGYMNVVRQAPGHGLEWIGYINPSRGYTNV 60
|||||
QY      61 AQKFGRTVMTDTSISTAYMELSLRSEDTRAIYCVRGFGYSYNDYYGMDVVGQGT 120
DB      61 NQKFRDRTVMTDTSFKSTAYMDLSRLSADSAAVYVCAR-----YYDHYCLDYVGQGT 114
|||||
QY      121 VTVSS 125
DB      115 VTVSS 119
|||||
RESULT 13
HVIG_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1991, sequence version 1.
DT 30-MAY-2006, entry version 38.
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
DE "Dispersed localization of D segments in the human immunoglobulin
DE heavy-chain locus."

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BX640625; CAE45779.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q6N091; 270-478.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41E4 CRC64;

Query Match 66.4%; Score 446; DB 2; Length 500;
Best Local Similarity 69.8%; Pred. No. 5.7e-36;
Matches 88; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY      1 QVQLVQSGAEVKPKGASVKVSCASGYTFTSYDINNVRQATQGLQGLWGMGWINPNSGNTDY 60
DB      38 QVQLVQSGAEVKPKGASVKVSCASGYTFTDHSITLWLRQAPGQGLWIGWISAYSGQTY 97
|||||
QY      61 AQKFGRTVMTDTSISTAYMELSLRSEDTRAIYCVRGFGY-SYNDYYGMDVVGQGT 119
DB      98 AQNLQGRVTMTDTSITAYMELSLRSDTTAVYYCAKQDSYTTIPNDAPH----IWQGT 154
|||||
QY      120 VTVSS 125
DB      155 VTVSS 160
|||||
RESULT 13
HVIG_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1991, sequence version 1.
DT 30-MAY-2006, entry version 38.
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
DE "Dispersed localization of D segments in the human immunoglobulin
DE heavy-chain locus."

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RL EMBL J. 7:1047-1051(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 20-116.
RX MEDLINE=93209281; PubMed=7681398;
RA Mariette X., Tsapis A., Brouet J.C.;
RT "Nucleotide sequence analysis of the variable domains of four human
RT monoclonal IgM with an antibody activity to myelin-associated
RT glycoprotein."
RL Eur. J. Immunol. 23:846-851(1993).
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
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CC
CC EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; S00476; HVH035.
DR HSP; P01751; INQB.
DR SMR; P23083; 20-117.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR LinkHub; P23083; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR03106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117 Ig heavy chain V-I region V35.
FT NON_TER 117 /FTID=PRO_0000015245.
FT FT
FT FT
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 65.6%; Score 441; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.5e-36;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db |||||
20 QVQLVQSGAEVKKPGASVKSCASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 79
|||

QY 61 AQKFGQVMTTRDTSISTAYMELSLRSEDYAIYCVR 98
Db |||||
80 AQKFGQVMTTRDTSISTAYMELSLRSDYTVYICAR 117
|||

RESULT 14
HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 43.
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
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CC
CC EMBL; J00240; AAA52988.1; -; Genomic_DNA.
DR PIR; A02024; HVH08.
DR HSP; P01751; INQB.
DR SMR; P01743; 20-117.
DR LinkHub; P01743; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR03106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117 Ig heavy chain V-I region HG3.
FT NON_TER 117 /FTID=PRO_0000015244.
FT FT
FT FT
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 65.5%; Score 440; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 4.4e-36;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKSCASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
Db |||||
20 QVQLVQSGAEVKKPGASVKSCASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 79
|||

QY 61 AQKFGQVMTTRDTSISTAYMELSLRSEDYAIYCVR 98
Db |||||
80 AQKFGQVMTTRDTSISTAYMELSLRSEDYTVYICAR 117
|||

RESULT 15
Q6P089_HUMAN PRELIMINARY; PRT; 480 AA.
ID Q6P089_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6P089;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 27-JUN-2006, entry version 21.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
```



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RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
NC  NUCLEOTIDE SEQUENCE.
RP  TISSUE=Glandular pool- thyroid;
RC  Strausberg R.;
RA  Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
RL  Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
CC  -I- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC  histocompatibility complex class I molecules [by similarity].
CC
CC
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC  -----
CC  EMBL; BC065733; AAH65733.1; -; mRNA.
CC
CC  HSSP; P01751; 1A6W.
CC
CC  SMR; Q6P089; 250-458.
CC
CC  GO; GO:0016021; C:integral to membrane; IEA.
CC
CC  GO; GO:0016020; C:membrane; IEA.
CC
CC  GO; GO:0030106; F:MHC class I receptor activity; IEA.
CC
CC  GO; GO:0013983; P:antigen presentation, endogenous antigen; IEA.
CC
CC  GO; GO:0013985; P:antigen processing, endogenous antigen via . . ; IEA.
CC
CC  InterPro; IPR007110; IG-like.
CC
CC  InterPro; IPR003597; IG_C1-set.
CC
CC  InterPro; IPR003006; IG_MHC.
CC
CC  InterPro; IPR003599; IG_sub.
CC
CC  InterPro; IPR013106; IG_V-set.
CC
CC  InterPro; IPR003596; IG_V-set_sub.
CC
CC  Pfam; PF07654; C1-set; 2.
CC
CC  Pfam; PF07686; V-set; 1.
CC
CC  SMART; SM00409; IG; 1.
CC
CC  SMART; SM00407; IGc1; 2.
CC
CC  SMART; SM00406; Igv; 1.
CC
CC  PROSITE; PS50835; IG_LIKE; 4.
CC
CC  PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW  Hypothetical protein; immunoglobulin domain; Membrane; Repeat;
KW  Transmembrane.
KW
SQ  SEQUENCE 480 AA; 51998 MW; 2E286C57E4F0ED65 CRC64;

Query Match          65.2%; Score 438; DB 2; Length 480;
Best Local Similarity 68.5%; Pred. No. 3.4e-35;
Matches 87; Conservative 13; Mismatches 19; Indels 8; Gaps

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Db  20  QYQLVQSGAEVKKTKTASVKVSKASGYISLDNYIHWRVQAQCGGLEWAWIRPQNGTYS 79
QY  61  AOKFQGRVTMTDRTISGTAYMELSLRSDDTAIYYCVRGFG--YSNYDYDYYGMDVWGQ 11
Db  80  ABEKFGQGVITITDTSINTAYMELTSLKSDTALYICARGHSDMSYFYD-----WGQG 13
QY  119  TTVTVSS 125
Db  134  TLTVTSS 140

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Search completed: April 25, 2007, 04:06:35
Job time : 85.0989 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 16 Seconds
(without alignments)
696.311 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB pep:*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB pep:*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB pep:*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB pep:*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB pep:*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB pep:*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541.5	80.6	120	2	US-09-025-769B-36 Sequence 36, Appl
2	541.5	80.6	120	2	US-09-025-769B-59 Sequence 59, Appl
3	541.5	80.6	120	2	US-09-490-070A-36 Sequence 36, Appl
4	541.5	80.6	120	2	US-09-490-070A-59 Sequence 59, Appl
5	541.5	80.6	120	2	US-09-490-153-36 Sequence 36, Appl
6	541.5	80.6	120	2	US-09-490-153-59 Sequence 59, Appl
7	541.5	80.6	120	2	US-09-490-324-36 Sequence 36, Appl
8	541.5	80.6	120	2	US-09-490-324-59 Sequence 59, Appl
9	528	78.6	117	2	US-09-025-769B-22 Sequence 22, Appl
10	528	78.6	117	2	US-09-490-070A-22 Sequence 22, Appl
11	528	78.6	117	2	US-09-490-153-22 Sequence 22, Appl
12	528	78.6	117	2	US-09-490-324-22 Sequence 22, Appl
13	526	78.3	470	2	US-09-859-053-28 Sequence 28, Appl
14	513	76.3	125	2	US-09-199-149-3 Sequence 3, Appl
15	510.5	76.0	128	1	US-08-202-047-22 Sequence 22, Appl
16	510.5	76.0	128	2	US-08-964-690-22 Sequence 22, Appl
17	510	75.9	129	1	US-08-561-521-45 Sequence 45, Appl
18	510	75.9	129	2	US-08-525-539A-77 Sequence 77, Appl
19	510	75.9	129	5	PCT-US95-01219-45 Sequence 45, Appl
20	504	75.0	123	2	US-10-330-613A-21 Sequence 21, Appl
21	502	74.7	123	1	US-08-477-877B-94 Sequence 94, Appl
22	502	74.7	123	1	US-08-472-281A-94 Sequence 94, Appl
23	502	74.7	123	1	US-08-477-989B-94 Sequence 94, Appl
24	502	74.7	123	2	US-09-462-140D-102 Sequence 102, App
25	502	74.7	123	2	US-09-462-140D-105 Sequence 105, App
26	501	74.6	119	1	US-08-561-521-10 Sequence 10, Appl

27	501	74.6	119	5	PCT-US95-01219-10 Sequence 10, Appl
28	498	74.1	119	2	US-09-438-954-41 Sequence 41, Appl
29	496	73.8	117	2	US-08-545-809A-96 Sequence 96, Appl
30	496	73.8	117	2	US-09-515-697-96 Sequence 96, Appl
31	493.5	73.4	139	1	US-08-253-877C-19 Sequence 19, Appl
32	493.5	73.4	139	1	US-08-452-164A-19 Sequence 19, Appl
33	493.5	73.4	139	2	US-08-603-024-18 Sequence 18, Appl
34	493.5	73.4	139	2	US-08-450-809-14 Sequence 14, Appl
35	487.5	72.5	118	3	US-09-875-221B-13 Sequence 13, Appl
36	487	72.5	96	2	US-10-194-975-3 Sequence 3, Appl
37	487	72.5	121	1	US-08-202-047-23 Sequence 23, Appl
38	487	72.5	121	2	US-08-964-690-23 Sequence 23, Appl
39	482	71.7	119	1	US-08-561-521-12 Sequence 12, Appl
40	482	71.7	119	5	PCT-US95-01219-12 Sequence 12, Appl
41	481	71.6	123	1	US-08-482-882-86 Sequence 86, Appl
42	481	71.6	123	1	US-08-483-389-86 Sequence 86, Appl
43	481	71.6	123	1	US-08-487-113D-86 Sequence 86, Appl
44	481	71.6	123	1	US-08-473-503-86 Sequence 86, Appl
45	481	71.6	123	1	US-08-483-932-86 Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-36
; Sequence 36, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.9e-44;

Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Qy 61 AQKFGQGVMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120
 Db 61 AQKFGQGVMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120
 Qy 121 VTVSS 125
 Db 116 VTVSS 120

RESULT 2

US-09-025-769B-59
 ; Sequence 59, Application US/09025769B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 59:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-025-769B-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.9e-44;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;
 Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Qy 61 AQKFGQGVMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120
 Db 61 AQKFGQGVMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120

Qy 121 VTVSS 125
 Db 116 VTVSS 120

RESULT 3

US-09-490-070A-36
 ; Sequence 36, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,070A
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colin G. Sandercock, Esq.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 37629-0005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 912-2000
 ; TELEFAX: (202) 912-2020
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 ; US-09-490-070A-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;
 Best Local Similarity 84.0%; Pred. No. 1.9e-44;
 Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;
 Qy 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Db 1 QVOLVSGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
 Qy 61 AQKFGQGVMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120
 Db 61 AQKFGQGVMTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGSYNYDYVGMVWGQGT 120
 Qy 121 VTVSS 125
 Db 116 VTVSS 120
 RESULT 4
 US-09-490-070A-59

; Sequence 59, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim

Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 White & McAuliffe
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006

Query Match	80.6%;	Score 541.5;	DB 2;	Length 120;
Best Local Similarity	84.0%;	Pred. NO. 1.9e-44;		
Matches 105:	Conservative	5.	Mismatch	10.
			Indel	5.

RESULT 5
US-09-490-153-36
; Sequence 36, Application US/09490153
; Patent No. 6706484
; GENERAL APPLICANT:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moronev, Simon

Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

Query Match	80.6%;	Score 541.5;	DB 2;	Length 120;
Best Local Similarity	84.0%;	Pred. No. 1.9e-44;		
Matches 105: Conservative	5;	Mismatches 10;	Indels 5;	Gaps 1;

RESULT 6
US-09-490-153-59
; Sequence 59, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim

Flueckmann, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas

/: CITY: New York
/: STATE: New York
/: COUNTRY: USA
/: ZIP: 10021
/:
/: COMPUTER READABLE FORM:
/: MEDIUM TYPE: Floppy disk
/: COMPUTER: IBM PC compatible
/: OPERATING SYSTEM: PC-DOS/MS-DOS
/: SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
/:
/: CURRENT APPLICATION DATA:
/: APPLICATION NUMBER: US/09/490,153
/: FILING DATE: 24-Jan-2000
/:
/: PRIOR APPLICATION DATA:
/: APPLICATION NUMBER: US/09/025,769B
/: FILING DATE: 18-FEB-1998
/: APPLICATION NUMBER: EP 95 11 3021.0
/: FILING DATE: 18-AUG-1995
/:
/: ATTORNEY/AGENT INFORMATION:
/: NAME: James F. Haley, Jr., Esq.
/: REGISTRATION NUMBER: 27,794
/: REFERENCE/DOCKET NUMBER: MORPHO/5
/: TELECOMMUNICATION INFORMATION:
/: TELEPHONE: (212)596-9000
/: TELEFAX: (212)596-9090
/:
/: INFORMATION FOR SEQ ID NO: 59:
/: SEQUENCE CHARACTERISTICS:
/: LENGTH: 120 amino acids
/: TYPE: amino acid
/: TOPOLOGY: linear
/: MOLECULE TYPE: protein
/: SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-153-59

Query Match 80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVROATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVROAPGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120

QY 121 VTVSS 125
Db 116 VTVSS 120

RESULT 7
US-09-490-324-36
; Sequence 36, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:

/: OPERATING SYSTEM: PC-DOS/MS-DOS
/: SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
/:
/: CURRENT APPLICATION DATA:
/: APPLICATION NUMBER: US/09/490,324
/: FILING DATE: 24-Jan-2000
/:
/: PRIOR APPLICATION DATA:
/: APPLICATION NUMBER: US/09/025,769
/: FILING DATE: 18-FEB-1998
/: APPLICATION NUMBER: EP 95 11 3021.0
/: FILING DATE: 18-AUG-1995
/:
/: ATTORNEY/AGENT INFORMATION:
/: NAME: James F. Haley, Jr., Esq.
/: REGISTRATION NUMBER: 27,794
/: REFERENCE/DOCKET NUMBER: MORPHO/5
/: TELECOMMUNICATION INFORMATION:
/: TELEPHONE: (212)596-9000
/: TELEFAX: (212)596-9090
/:
/: INFORMATION FOR SEQ ID NO: 36:
/: SEQUENCE CHARACTERISTICS:
/: LENGTH: 120 amino acids
/: TYPE: amino acid
/: STRANDEDNESS: <unknown>
/: TOPOLOGY: linear
/: MOLECULE TYPE: protein
/: SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-324-36

Query Match 80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVROATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVROAPGQGLEWMGWINPNSGGTNY 60

QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYCVRGFGYSYNDYYGMDVWGQGT 120

QY 121 VTVSS 125
Db 116 VTVSS 120

RESULT 8
US-09-490-324-59
; Sequence 59, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9000
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-324-59

Query Match      80.6%; Score 541.5; DB 2; Length 120;
Best Local Similarity 84.0%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTDY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 115
QY 121 VTVSS 125
Db 116 VTVSS 120

RESULT 9
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:

; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <unknown>
; TOPOLOGY: linear

; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-22

Query Match      78.6%; Score 528; DB 2; Length 117;
Best Local Similarity 82.5%; Pred. No. 3.5e-43;
Matches 104; Conservative 5; Mismatches 7; Indels 10; Gaps 2;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTDY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 119
Db 61 AQKFGQRTVMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 111
QY 120 VTVSS 125
Db 112 VTVSS 117

RESULT 10
US-09-490-070A-22
; Sequence 22, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <unknown>
; TOPOLOGY: linear
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Query Match	78.6%;	Score 528;	DB 2;	Length 117;
Best Local Similarity	82.5%;	Pred. No. 3.5e-43;		

QY 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
 Db 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCARDGDG-----GFDYWGQGT 111
 QY 120 TVTVSS 125
 Db 112 LTVVSS 117

RESULT 13
 US-09-859-053-28
 ; Sequence 28, Application US/09859053
 ; Patent No. 6803039
 ; GENERAL INFORMATION:
 ; APPLICANT: Teuji, Takashi
 ; APPLICANT: Tezuka, Katsunari
 ; APPLICANT: Hori, No. 6803039uaki
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
 ; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
 ; FILE REFERENCE: 06501-079001
 ; CURRENT APPLICATION NUMBER: US/09/859,053
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: JP 2001-99508
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: JP 2000-147116
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-859-053-28

Query Match 78.3%; Score 526; DB 2; Length 470;
 Best Local Similarity 79.2%; Pred. No. 2.6e-42;
 Matches 99; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGCGLEWMGWINPNSGNTDY 60
 Db 20 QVOLVSGAEVKKPGASVKVSKASGYTFTGYMHWVRQAPGCGLEWMGWINPHSGGNTY 79
 QY 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
 Db 80 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCARDTYYDSGGYHDAFDWQGT 139
 QY 121 VTVSS 125
 Db 140 VTVSS 144

RESULT 14
 US-09-199-149-3
 ; Sequence 3, Application US/09199149
 ; Patent No. 6160099
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonak, Zdenka L.
 ; APPLICANT: Taylor, Alexander H.
 ; APPLICANT: Trulli Jr., Stephen H.
 ; APPLICANT: Johanson, Kyung O.
 ; TITLE OF INVENTION: Humanized Monoclonal Antibodies
 ; FILE REFERENCE: P50860
 ; CURRENT APPLICATION NUMBER: US/09/199,149
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Kabat VH subgroup I
 US-09-199-149-3

Query Match 76.3%; Score 513; DB 2; Length 125;
 Best Local Similarity 80.6%; Pred. No. 1e-41;
 Matches 104; Conservative 8; Mismatches 9; Indels 8; Gaps 5;
 QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGCGLEWMGWINPNSGNTDY 60
 Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYAISWVRQAPGCGLEWMGWINP-GGDTNY 59
 QY 61 AOKFQGRVTMTDTSISTAYMELSSLSRSDTAIYYCVR-GFGYS---YNDYYGMDVWG 116
 Db 60 AOKFQGRVTITADTSTSTAYMELSSLSRSDTAIYYCARPGYGGCGYGY-WYWG--VWG 116
 QY 117 QGTVTVSS 125
 Db 117 QGTVTVSS 125

RESULT 15
 US-08-202-047-22
 ; Sequence 22, Application US/08202047
 ; Patent No. 5800815
 ; GENERAL INFORMATION:
 ; APPLICANT: CHESNUT, Robert W.
 ; APPLICANT: POLLEY, Margaret J.
 ; APPLICANT: PAULSON, James C.
 ; APPLICANT: JONES, S. Tarran
 ; APPLICANT: SALDANHA, Jose W.
 ; APPLICANT: BENDIG, Mary M.
 ; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/202,047
 ; FILING DATE: 25-FEB-1994
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 14137-77
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 128 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..128
 ; OTHER INFORMATION: /label= HUMAN_I
 US-08-202-047-22

Query Match 76.0%; Score 510.5; DB 1; Length 128;
 Best Local Similarity 77.9%; Pred. No. 1.8e-41;
 Matches 102; Conservative 7; Mismatches 13; Indels 9; Gaps 3;
 QY 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGCGLEWMGWINP-NSGNTD 59
 Db 1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYAISWVRQAPGCGLEWMGWINPYNCGDNT 60

Qy	60	YAKFQGRVTTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYS-----YNYDYYYGMDV	114
Db	61	YAKFQGRVTITADTSTSTAYMELSSLRSEDTAIYYCARAPCGSGGGCYRGDYF---DY	117
Qy	115	WQGGTTTVTVSS	125
Db	118	WQGGTLTVTVSS	128

Search completed: April 25, 2007, 04:08:31
Job time : 16.7133 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 46 Seconds
(without alignments)
1251.741 Million cell updates/sec

Title: US-10-665-383-2

Perfect score: 672

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....YDYYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	672	100.0	125	4	US-10-041-860-48
2	672	100.0	125	4	US-10-041-860-200
3	672	100.0	125	4	US-10-041-860-237
4	672	100.0	125	4	US-10-041-860-372
5	672	100.0	125	4	US-10-665-383-2
6	638	94.9	125	4	US-10-041-860-38
7	638	94.9	125	4	US-10-041-860-203
8	638	94.9	125	4	US-10-041-860-240
9	638	94.9	125	4	US-10-041-860-343
10	638	94.9	125	4	US-10-665-383-54
11	593.5	88.3	126	4	US-10-041-860-19
12	593.5	88.3	126	4	US-10-041-860-201
13	593.5	88.3	126	4	US-10-041-860-208
14	593.5	88.3	126	4	US-10-665-383-18
15	579.5	86.2	125	4	US-10-041-860-238
16	575.5	85.6	126	4	US-10-041-860-40
17	575.5	85.6	126	4	US-10-041-860-204
18	575.5	85.6	126	4	US-10-041-860-241
19	575.5	85.6	126	4	US-10-041-860-349
20	575.5	85.6	126	4	US-10-665-383-58
21	572	85.1	127	4	US-10-041-860-44
22	572	85.1	127	4	US-10-041-860-205
23	572	85.1	127	4	US-10-041-860-242
24	572	85.1	127	4	US-10-041-860-360
25	572	85.1	127	4	US-10-665-383-66
26	567.5	84.4	126	4	US-10-041-860-21
27	567.5	84.4	126	4	US-10-041-860-199

28	567.5	84.4	126	4	US-10-041-860-236	Sequence 236, App
29	567.5	84.4	126	4	US-10-041-860-294	Sequence 294, App
30	567.5	84.4	126	4	US-10-665-383-22	Sequence 22, Appl
31	562.5	83.7	124	4	US-10-309-762-125	Sequence 125, App
32	561.5	83.6	122	4	US-10-269-805-61	Sequence 61, Appl
33	561.5	83.6	122	5	US-10-982-440-61	Sequence 61, Appl
34	561.5	83.6	126	4	US-10-041-860-37	Sequence 37, Appl
35	561.5	83.6	126	4	US-10-041-860-202	Sequence 202, App
36	561.5	83.6	126	4	US-10-041-860-239	Sequence 239, App
37	561.5	83.6	126	4	US-10-665-383-74	Sequence 74, Appl
38	558.5	83.1	145	4	US-10-478-056-29	Sequence 29, Appl
39	558.5	83.1	145	5	US-10-721-763-29	Sequence 29, Appl
40	554	82.4	125	5	US-10-727-155-162	Sequence 162, App
41	553.5	82.4	126	5	US-10-734-661A-101	Sequence 101, App
42	551.5	82.1	118	4	US-10-309-762-124	Sequence 124, App
43	551	82.0	127	5	US-10-734-661A-103	Sequence 103, App
44	548.5	81.6	255	6	US-11-030-847-79	Sequence 79, Appl
45	547.5	81.5	128	4	US-10-371-942-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-10-041-860-48

; Sequence 48, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ARGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 48

; LENGTH: 125

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-48

Query Match 100.0%; Score 672; DB 4; Length 125;

Best Local Similarity 100.0%; Pred. No. 9.5e-54;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLVWGWINPNSGNTDY 60

Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLVWGWINPNSGNTDY 60

Qy 61 AQKFGQRTVTRDTSISTAYMELSSLSSEPTAIYVCVRGFGYSYNDYYGMDVWGQGT 120

Db 61 AQKFGQRTVTRDTSISTAYMELSSLSSEPTAIYVCVRGFGYSYNDYYGMDVWGQGT 120

Qy 121 VTSS 125

Db 121 VTSS 125

RESULT 2

US-10-041-860-200

; Sequence 200, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

```
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-200

Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 3
US-10-041-860-237
; Sequence 237, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-237

Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 4
US-10-041-860-372
; Sequence 372, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372

Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQGRVTMTTRDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 5
US-10-665-383-2
; Sequence 2, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-2
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Query Match      100.0%; Score 672; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 9.5e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 6
US-10-041-860-38
; Sequence 38, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-38

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
US-10-041-860-203
; Sequence 203, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-38

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 8
US-10-041-860-240
; Sequence 240, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-240

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

```

```

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-203

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 8
US-10-041-860-240
; Sequence 240, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-240

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
QY 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
DB 61 AQKFGQRTVMTDTSISTAYMELSLRSSEDTAIYVCVRGFGSYNYDYGGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

```

```

RESULT 9
US-10-041-860-343
; Sequence 343, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-343

Query Match      94.9%; Score 638; DB 4; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.2e-50;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVVRQATGQGLEWMGNPNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVVRQATGQGLEWMGNPNPNSGNTGY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AQKFGQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNDYYGMDVWGQGT 120

QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 11
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVVRQATGQGLEWMGNPNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVVRQATGQGLEWMGNPNPNSGNTGY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQGRVTMTSDTSISTAYMELSSLRSEDTAIYYCAREGIAVAGTYYYYYGMVDWGQGT 120

QY 120 TVTVSS 125
DB 121 TVTVSS 126

RESULT 12
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
```

```
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120

QY 120 TTVTVSS 125
DB 121 TTVTVSS 126

RESULT 13
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120

QY 120 TTVTVSS 125
DB 121 TTVTVSS 126

RESULT 14
US-10-665-383-18
; Sequence 18, Application US/10665383
; Publication No. US20040141969A1

; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-18

Query Match      88.3%; Score 593.5; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.5e-46;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGY 60

QY 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 119
DB 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 120

QY 120 TTVTVSS 125
DB 121 TTVTVSS 126

RESULT 15
US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match      86.2%; Score 579.5; DB 4; Length 125;
Best Local Similarity 89.4%; Pred. No. 2.7e-45;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 LVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTDYAQK 63
DB 3 LVQSGAEVKKPGASVKVSKASGYTFTSYDINNVRQATGQGLEWMGWINPNSGNTGYAQK 62

QY 64 PQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNDYYGMDVWGQGT 122
```

Db 63 FQGRVTMTNTSISITAYMELSSLRSEDATVYCAREGIAVAGTYYYYYGVNDVWGQTTVT 122

QY 123 VSS 125

Db 123 VSS 125

Search completed: April 25, 2007, 04:22:50
Job time : 47.2571 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 48 Seconds
(without alignments)
533.620 Million cell updates/sec

Title: US-10-665-383-2
Perfect score: 672
Sequence: 1 QVOLVQSGAEVKKPGASVKV.....YDYRYGMDVWGQGTITVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	672	100.0	125	7 US-11-109-181-48	Sequence 48, Appl
2	672	100.0	125	7 US-11-109-181-200	Sequence 200, Appl
3	672	100.0	125	7 US-11-109-181-237	Sequence 237, Appl
4	672	100.0	125	7 US-11-109-181-372	Sequence 372, Appl
5	638	94.9	125	7 US-11-109-181-38	Sequence 38, Appl
6	638	94.9	125	7 US-11-109-181-203	Sequence 203, Appl
7	638	94.9	125	7 US-11-109-181-240	Sequence 240, Appl
8	638	94.9	125	7 US-11-109-181-343	Sequence 343, Appl
9	599	89.1	126	7 US-11-433-924-94	Sequence 94, Appl
10	593.5	88.3	126	7 US-11-109-181-19	Sequence 19, Appl
11	593.5	88.3	126	7 US-11-109-181-201	Sequence 201, Appl
12	593.5	88.3	126	7 US-11-109-181-288	Sequence 288, Appl
13	579.5	86.2	125	7 US-11-109-181-238	Sequence 238, Appl
14	576.5	85.8	122	7 US-11-433-924-234	Sequence 234, Appl
15	575.5	85.6	126	7 US-11-109-181-40	Sequence 40, Appl
16	575.5	85.6	126	7 US-11-109-181-204	Sequence 204, Appl
17	575.5	85.6	126	7 US-11-109-181-241	Sequence 241, Appl
18	575.5	85.6	126	7 US-11-109-181-349	Sequence 349, Appl
19	572	85.1	127	7 US-11-109-181-44	Sequence 44, Appl
20	572	85.1	127	7 US-11-109-181-205	Sequence 205, Appl
21	572	85.1	127	7 US-11-109-181-242	Sequence 242, Appl
22	572	85.1	127	7 US-11-109-181-360	Sequence 360, Appl
23	570	84.8	126	7 US-11-311-939-425	Sequence 425, Appl
24	570	84.8	126	7 US-11-311-939-429	Sequence 429, Appl
25	567.5	84.4	126	7 US-11-109-181-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-11-109-181-48
; Sequence 48, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao-Dong
; APPLICANT: Yang, Francine
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-48

Query Match 100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.9e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QVOLVQSGAEVKKPGASVKVSCASGYTFTSYDINWYRQATGQGLEWGWINPNSGNTDY	60
DB	1	QVOLVQSGAEVKKPGASVKVSCASGYTFTSYDINWYRQATGQGLEWGWINPNSGNTDY	60
QY	61	AKQFQGRVTMTRTSISTATMELSSLRSEDTAIYCVRGFGYSNYYDYGMVWGQGT	120
DB	61	AKQFQGRVTMTRTSISTATMELSSLRSEDTAIYCVRGFGYSNYYDYGMVWGQGT	120
QY	121	VTVSS	125
DB	121	VTVSS	125

RESULT 2

US-11-109-181-200
; Sequence 200, Application US/11109181


```
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-200

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.9e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVROATGQGLEWMGWINPNSGNTDY 60
      |||
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVROATGQGLEWMGWINPNSGNTDY 60
      |||

QY      61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
      |||
Db      61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
      |||

QY      121 VTVSS 125
      |||
Db      121 VTVSS 125
      |||

RESULT 4
US-11-109-181-372
; Sequence 372, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-372

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.9e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVROATGQGLEWMGWINPNSGNTDY 60
      |||
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVROATGQGLEWMGWINPNSGNTDY 60
      |||

QY      61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
      |||
Db      61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYDYGGMDVWGQGT 120
      |||

QY      121 VTVSS 125
      |||
Db      121 VTVSS 125
      |||

RESULT 5
US-11-109-181-38
; Sequence 38, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-237

Query Match      100.0%; Score 672; DB 7; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.9e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-38

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATQCGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATQCGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCARGSGYSYGYDYYGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 6
US-11-109-181-203
; Sequence 203, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-203

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATQCGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATQCGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCARGSGYSYGYDYYGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 7
US-11-109-181-240
; Sequence 240, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-240

Query Match          94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATQCGLEWGMWNPNSGNTDY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINNVQRATQCGLEWGMWNPNSGNTGY 60
QY 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCVRGFGYSYNDYYGMDVWGQGT 120
DB 61 AOKFQGRVTMTDTSISTAYMELSLRSEDTAIYVCARGSGYSYGYDYYGMDVWGQGT 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 8
US-11-109-181-343
; Sequence 343, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 125
; TYPE: PRT
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; ORGANISM: homo sapiens
US-11-109-181-343

Query Match      94.9%; Score 638; DB 7; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.3e-52;
Matches 118; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYNDYYGMDVWGQTT 120
Db 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGFGSYNYNDYYGMDVWGQTT 120

Qy 121 TVTVSS 125
Db 121 TVTVSS 125

RESULT 9
US-11-433-924-94
; Sequence 94, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Almee
; APPLICANT: Poord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-94

Query Match      89.1%; Score 599; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.9e-49;
Matches 113; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGFGVSY--NYDYIYGMVWGQ 118
Db 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGFGVSSWYRGYYIYGMVWGQ 120

Qy 119 TTVTVS 124
Db 121 TTVTVS 126

RESULT 10
US-11-109-181-19
; Sequence 19, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi

; ORGANISM: homo sapiens
US-11-109-181-19

Query Match      88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 2e-48;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNYDYIYGMVWGQGT 119
Db 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGAGIAGTAYIYIYGMVWGQGT 120
```

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; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR APPLICATION NUMBER: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-19

Query Match      88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 2e-48;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNYDYIYGMVWGQGT 119
Db 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGAGIAGTAYIYIYGMVWGQGT 120

Qy 120 TTVTVS 125
Db 121 TTVTVS 126

RESULT 11
US-11-109-181-201
; Sequence 201, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-201

Query Match      88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 2e-48;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTGY 60

Qy 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVR-GFGYSYNYDYIYGMVWGQGT 119
Db 61 AQKFGQRTVMTSDTSISTAYMELSLRSEDTAIYYCVRGAGIAGTAYIYIYGMVWGQGT 120
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; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-238

Query Match      86.2%; Score 579.5; DB 7; Length 125;
Best Local Similarity 89.4%; Pred. No. 4e-47;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDYAQK 63
   |||||
DB 3 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGYAQK 62
   |||||

QY 64 FQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSYNYDYYGMDVWGQGT 122
   |||||
DB 63 FQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 122
   |||||

QY 123 VSS 125
   |||
DB 123 VSS 125
   |||

RESULT 14
US-11-433-924-254
; Sequence 254, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sird-Aimee
; APPLICANT: Foord, Oric
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-254

Query Match      85.8%; Score 576.5; DB 7; Length 122;
Best Local Similarity 87.4%; Pred. No. 7.6e-47;
Matches 111; Conservative 5; Mismatches 4; Indels 7; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDY 60
   |||||
DB 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGY 60
   |||||

QY 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSYNYDYY--GMDVWGQ 118
   |||||
DB 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCARNW-----DFYDFGMDVWGQ 115
   |||||

QY 119 TTVTVSS 125
   |||||
DB 116 TTVTVSS 122
   |||||

RESULT 15
US-11-109-181-40
; Sequence 40, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-288

Query Match      88.3%; Score 593.5; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 2e-48;
Matches 113; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDY 60
   |||||
DB 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGY 60
   |||||

QY 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSYNYDYYGMDVWGQGT 119
   |||||
DB 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 120
   |||||

QY 120 TTVTVSS 125
   |||||
DB 121 TTVTVSS 126
   |||||

RESULT 13
US-11-109-181-238
; Sequence 238, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-238

Query Match      86.2%; Score 579.5; DB 7; Length 125;
Best Local Similarity 89.4%; Pred. No. 4e-47;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDYAQK 63
   |||||
DB 3 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGYAQK 62
   |||||

QY 64 FQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSYNYDYYGMDVWGQGT 122
   |||||
DB 63 FQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 122
   |||||

QY 123 VSS 125
   |||
DB 123 VSS 125
   |||

RESULT 14
US-11-433-924-254
; Sequence 254, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sird-Aimee
; APPLICANT: Foord, Oric
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-254

Query Match      85.8%; Score 576.5; DB 7; Length 122;
Best Local Similarity 87.4%; Pred. No. 7.6e-47;
Matches 111; Conservative 5; Mismatches 4; Indels 7; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDY 60
   |||||
DB 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGY 60
   |||||

QY 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSYNYDYY--GMDVWGQ 118
   |||||
DB 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCARNW-----DFYDFGMDVWGQ 115
   |||||

QY 119 TTVTVSS 125
   |||||
DB 116 TTVTVSS 122
   |||||

RESULT 15
US-11-109-181-40
; Sequence 40, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-238

Query Match      86.2%; Score 579.5; DB 7; Length 125;
Best Local Similarity 89.4%; Pred. No. 4e-47;
Matches 110; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDYAQK 63
   |||||
DB 3 LVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGYAQK 62
   |||||

QY 64 FQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVR-GFGYSYNYDYYGMDVWGQGT 122
   |||||
DB 63 FQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCAREGIAVAGTYYYYYGMVWGQGT 122
   |||||

QY 123 VSS 125
   |||
DB 123 VSS 125
   |||

RESULT 14
US-11-433-924-254
; Sequence 254, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sird-Aimee
; APPLICANT: Foord, Oric
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-254

Query Match      85.8%; Score 576.5; DB 7; Length 122;
Best Local Similarity 87.4%; Pred. No. 7.6e-47;
Matches 111; Conservative 5; Mismatches 4; Indels 7; Gaps 2;

QY 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTDY 60
   |||||
DB 1 QVQLVQSGAEVKKPGASVKSCASGYFTSYDINWVRQATQGLEWGWGWINPNSGNTGY 60
   |||||

QY 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCVRGFGYSYNYDYY--GMDVWGQ 118
   |||||
DB 61 AOKFQGRVTMTTRDTSISTAYMELSLRSRSDTAIYYCARNW-----DFYDFGMDVWGQ 115
   |||||

QY 119 TTVTVSS 125
   |||||

```

APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-40

Query Match 85.6%; Score 575.5; DB 7; Length 126;
Best Local Similarity 87.3%; Pred. No. 9.7e-47;
Matches 110; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
Qy 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATQCGLEWGMWINPNSGNTDY 60
Db 1 QVQLVQSGAEVKKPKGASVKVSKASGYTFTSYDINWVRQATQCGLEWGMWINPNSGNTGY 60
Qy 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYN-YDYIYGMVDVWGQGT 119
Db 61 AQKFGQGRVTMTSDTSISTAYMELSLRSEDTAIYYCVRGFGYSYN-YDYIYGMVDVWGQGT 120
Qy 120 TTVTVSS 125
Db 121 TTVTVSS 126

Search completed: April 25, 2007, 04:27:43
Job time : 48.1992 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 94 Seconds
(without alignments)
564.248 Million cell updates/sec

Title: US-10-665-383-4
Perfect score: 558
Sequence: 1 EIVLQSPGTLSPGERAT.....COQYGSPSCFQGTGLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*
11: Geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	108	7 ADK18625	Adk18625 Anti-huma
2	558	100.0	108	7 ADK18951	Adk18951 Anti-huma
3	558	100.0	108	7 ADK18835	Adk18835 Anti-huma
4	558	100.0	108	7 ADK18801	Adk18801 Anti-huma
5	558	100.0	108	8 ADL25394	Adl25394 Human mAb
6	543	97.3	109	10 AEF73695	Aef73695 Human IL-
7	543	97.3	236	10 AEF73710	Aef73710 Human IL-
8	535	95.9	108	9 ADY26769	Ady26769 Anti-NGF-
9	535	95.9	108	9 ADY26816	Ady26816 Human ant
10	535	95.9	128	9 AD257709	Ad257709 Germline
11	535	95.9	129	2 AAR38672	Aar38672 vK325-Jk2
12	533	95.5	108	7 ADP03986	Adp03986 Murine-ex
13	533	95.5	120	10 AEH89253	Aeh89253 Anti-VEGF
14	533	95.5	130	6 ABJ36930	Abj36930 Anti-CD40
15	533	95.5	130	10 AEG95253	Aeg95253 Human imm
16	533	95.5	140	10 AEH89279	Aeh89279 Anti-VRGF
17	533	95.5	384	4 AMZ4101	Aam4101 Human EST
18	532	95.3	108	8 ADQ16703	Adq16703 Modified
19	532	95.3	108	9 ADV44439	Adv44439 pAX116 va
20	532	95.3	108	9 AEB12911	Aeb12911 Antibody
21	532	95.3	108	9 AEC81271	Aec81271 Human mon
22	532	95.3	108	9 AEC81269	Aec81269 Human mon

23	532	95.3	108	9 AEC81267	Aec81267 Human mon
24	532	95.3	108	10 AEF81808	Aef81808 Human ant
25	532	95.3	108	10 AEF81806	Aef81806 Human ant
26	532	95.3	108	10 AEF81804	Aef81804 Human ant
27	532	95.3	109	8 ADP46971	Adp46971 Murine li
28	532	95.3	109	10 AEF65167	Aef65167 Anti-Ang-
29	532	95.3	112	9 ADV44477	Adv44477 Anti-teta
30	532	95.3	115	10 AEE03759	Aee03759 Antibody
31	532	95.3	120	7 ADD40551	Add40551 3E1/4G11
32	532	95.3	130	9 AEB12948	Aeb12948 Antibody
33	532	95.3	215	8 ADQ16702	Adq16702 Modified
34	532	95.3	215	9 ADV44438	Adv44438 PAX116 va
35	532	95.3	215	9 AEB12910	Aeb12910 Antibody
36	532	95.3	239	9 ADV44458	Adv44458 Anti-teta
37	532	95.3	239	9 AEB12929	Aeb12929 Antibody
38	531	95.2	108	9 ADZ42030	Adz42030 Ig L chai
39	531	95.2	108	9 ADZ42032	Adz42032 Ig L chai
40	531	95.2	108	9 ADZ42034	Adz42034 Ig L chai
41	531	95.2	108	9 AEA89845	Aea89845 Anti-IFN
42	530	95.0	384	4 AAU14462	Aau14462 Human nov
43	530	95.0	384	4 AAU14463	Aau14463 Human nov
44	530	95.0	384	4 AAU14461	Aau14461 Human nov
45	530	95.0	384	4 AAU14464	Aau14464 Human nov

ALIGNMENTS

RESULT 1
ADK18625
ID ADK18625 standard; protein; 108 AA.
AC ADK18625;
XX
DT 06-MAY-2004 (first entry)
DE Anti-human PDGF-D antibody light chain protein sequence.
XX
XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX Homo sapiens.
XX
XX WO2003057857-A2.
XX
XX PD 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
XX 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 49; 255pp; English.

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
 |||||
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
 |||||

QY 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||
 DB 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||

RESULT 2
 ADK18951
 ID ADK18951 standard; protein; 108 AA.
 AC ADK18951;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody protein related sequence #177.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057857-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 XX
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 PT New human monoclonal antibody that binds to platelet-derived growth
 factor-D (PDGF-D), useful for treating chronic and recurrent human
 diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 375; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to
 platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 treating chronic and recurrent human diseases, such as inflammation,
 autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 useful for modulating collagen formation, and for staging various
 cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 generated using an active protein fragment of the gene product from the
 clone 30664188.0.99 arising in the conditioned medium obtained when
 HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 sequence corresponds to a protein used in the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
 |||||
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
 |||||

QY 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||
 DB 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||

DB 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||

RESULT 3
 ADK18835
 ID ADK18835 standard; protein; 108 AA.
 AC ADK18835;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody protein related sequence #61.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057857-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 XX
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 PT New human monoclonal antibody that binds to platelet-derived growth
 factor-D (PDGF-D), useful for treating chronic and recurrent human
 diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 259; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to
 platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 treating chronic and recurrent human diseases, such as inflammation,
 autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 useful for modulating collagen formation, and for staging various
 cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 generated using an active protein fragment of the gene product from the
 clone 30664188.0.99 arising in the conditioned medium obtained when
 HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 sequence corresponds to a protein used in the invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 558; DB 7; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
 |||||
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQAPRLLIYATSSRATGIP 60
 |||||

QY 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||
 DB 61 DRFSGSGGTDTLTISRLEPEDPAVYCCQYGGSSPCSGGQTKLEIK 108
 |||||

RESULT 4
 ADK18801
 ID ADK18801 standard; protein; 108 AA.
 AC ADK18801;
 XX
 DT 06-MAY-2004 (first entry)
 XX

DE Anti-human PDGF-D antibody protein related sequence #27.
 XX antiinflammatory; immunomodulator; cytostatic; gene therapy.
 KW Homo sapiens.
 OS WO2003057857-A2.
 XX 17-JUL-2003.
 XX 06-JAN-2003; 2003WO-US000398.
 XX 07-JAN-2002; 2002US-00041860.
 XX (ABGE-) ABGENIX INC.
 PA Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX WPI; 2003-587119/55.
 DR New human monoclonal antibody that binds to platelet-derived growth
 XX factor-D (PDGF-D), useful for treating chronic and recurrent human
 XX diseases, such as inflammation, autoimmunity and cancer.
 XX Disclosure; SEQ ID NO 225; 255pp; English.
 XX The invention relates to a human monoclonal antibody that binds to
 CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 CC treating chronic and recurrent human diseases, such as inflammation,
 CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 CC useful for modulating collagen formation, and for staging various
 CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 CC generated using an active protein fragment of the gene product from the
 CC clone 30664188.0.99 arising in the conditioned medium obtained when
 CC HBK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 CC sequence corresponds to a protein used in the invention.
 XX Sequence 108 AA;
 SQ
 Query Match 100.0%; Score 558; DB 7; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
 QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYSSPCSPFGQGTGLEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYSSPCSPFGQGTGLEIK 108
 RESULT 5
 ADL25394
 ID ADL25394 standard; protein; 108 AA.
 XX
 AC ADL25394;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human mAb 6.4 light chain variable region protein SEQ ID NO:4.
 XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
 KW nephritis; mesangial cell proliferation inhibition;
 KW mesangial proliferative glomerulonephritis; nephrotropic;
 KW antinflammatory; dermatological; immunosuppressive; antidiabetic;
 KW Gene therapy; human; monoclonal antibody; mAb.
 XX Homo sapiens.
 OS WO2004024098-A2.
 PN
 XX

PD 25-MAR-2004.
 XX 16-SEP-2003; 2003WO-US029414.
 XX 16-SEP-2002; 2002US-0411137P.
 XX (ABGE-) ABGENIX INC.
 PA (CURA-) CURAGEN CORP.
 XX Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
 XX WPI; 2004-269881/25.
 DR N-PSDB; ADL25393.
 XX Use of an antibody or its binding fragment that binds platelet derived
 XX growth factor-DD (PDGF-DD) for preparing a medicament for treating
 XX nephritis.
 XX Disclosure; SEQ ID NO 4; 115pp; English.
 XX The present invention describes an antibody or its binding fragment that
 CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
 CC useful in preparing a medicament for treating nephritis. Also described:
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
 CC of treating mesangial proliferative glomerulonephritis. The antibody has
 CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
 CC antidiabetic activities, and can be used in gene therapy. The antibody or
 CC its binding fragment, that binds PDGF-DD, can be used in preparing a
 CC medicament for treating nephritis and related disorders, e.g., mesangial
 CC proliferative glomerulonephritis. The present sequence represents a human
 CC monoclonal antibody (mAb) variable region sequence, which is used in the
 CC exemplification of the present invention.
 XX Sequence 108 AA;
 SQ
 Query Match 100.0%; Score 558; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.6e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
 QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYSSPCSPFGQGTGLEIK 108
 DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYSSPCSPFGQGTGLEIK 108
 RESULT 6
 AEF73695
 ID AEF73695 standard; protein; 109 AA.
 XX
 AC AEF73695;
 XX
 DT 06-APR-2006 (first entry)
 XX
 DE Human IL-17 antibody AIN457 light chain variable region.
 XX Interleukin-17 antagonist; antibody production; antibody therapy;
 KW osteoarthritis; rheumatoid arthritis; osteoporosis; inflammation;
 KW antiarthritic; antirheumatic; osteopathic; antinflammatory;
 KW musculoskeletal disease; immune disorder; inflammation; degeneration;
 KW endocrine disease; light chain variable region.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Region 24..35
 FT /label= L-CDR1
 FT Region 51..57
 FT /label= L-CDR2
 FT Region 90..98

FT XX WO2006013107-A1. /label= L-CDR3

PN XX

XX XX

PD XX 09-FEB-2006.

PF XX 04-AUG-2005; 2005WO-EP008470.

PR XX 05-AUG-2004; 2004GB-00017487.

XX XX (NOVS) NOVARTIS AG.

PA XX (NOVS) NOVARTIS PHARMA GMBH.

XX XX

PI PI Di Padova FE, Gram H, Hofstetter H, Jeschke M, Rondeau J;

PI PI Van Den Berg W;

XX XX

DR WPI; 2006-145760/15.

DR N-PSDB; AEF73694.

XX XX

PT Novel interleukin-17 binding molecule capable of inhibiting human IL-17

PT activity and IL-6 production induced by human-IL-17 in human dermal

PT fibroblasts, useful for treating IL-mediated diseases e.g.

PT osteoarthritis.

XX XX

PS Claim 5; SEQ ID NO 10; 76pp; English.

XX XX

CC The present invention relates to interleukin-17 (IL-17) antagonistic

CC antibodies suitable for use in the treatment of IL-17 mediated diseases

CC and disorders. A claimed IL-17 binding molecule is capable of inhibiting

CC the activity of 1 nM human IL-17 at a concentration of less than 5 nM by

CC 50%, the activity being measured on interleukin-6 production induced by

CC human IL-17 in human dermal fibroblasts. The IL-17 binding molecule

CC comprises: a heavy chain variable region (VH) comprising complementarity

CC determining regions CDR1, CDR2 and CDR3 AEF73686-AEF73688 or CDR1-x, CDR2

CC -x and CDR3-x AEF73696-AEF73698 from anti-human IL-17 antibody AIN457;

CC and a light chain variable region (LH) comprising CDR1', CDR2' and CDR3'

CC AEF73689-AEF73691 from AIN457. The IL-17 binding molecule is preferably a

CC human antibody. It preferably comprises at least one antigen binding site

CC comprising a first domain having amino acid sequence homology to the

CC AIN457 VH region AEF73693 and a second domain having amino acid sequence

CC homology to the AIN457 VL region AEF73695. Also provided are a DNA

CC construct encoding the IL-17 binding molecules of the invention, an

CC expression vector comprising the DNA construct, and a method of producing

CC an IL-17 binding molecule by culturing a transformed host cell line. The

CC IL-17 binding molecule is used to manufacture a medicament for the

CC treatment of an IL-17 mediated disease or disorder, especially

CC osteoarthritis, rheumatoid arthritis, osteoporosis and other inflammatory

CC arthritides. In an example from the invention, transgenic mouse 27340,

CC which is engineered to express the human IgG/kappa repertoire instead of

CC the murine immunoglobulin repertoire, was used to generate antibodies to

CC human IL-17. B-cells from these mice were immortalized by standard

CC hybridoma technology and murine hybridoma cells were obtained which

CC secreted the human IgG1/kappa antibody AIN457. The present sequence is

XX the amino acid sequence of AIN457 VL.

XX XX

SQ Sequence 109 AA;

Query Match 97.3%; Score 543; DB 10; Length 109;

Best Local Similarity 96.3%; Pred. No. 6.4e-34;

Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYYATSSRATGIP 60

DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIYYATSSRATGIP 60

QY 61 DRFSGSGSTDTLTISRLEPEDFAVYYCQQYGSSPCSPGQGTKLEIK 108

DB 61 DRFSGSGSGTDTLTISRLEPEDFAVYYCQQYGSSPCSPGQGTKLEIK 108

RESULT 7

AEF73710

ID AEF73710 standard; protein; 236 AA.

XX AEF73710;

AC XX

DT 06-APR-2006 (first entry)

XX XX

DE Human IL-17 antibody AIN457 light chain.

XX XX

KW Interleukin-17 antagonist; antibody production; antibody therapy;

KW osteoarthritis; rheumatoid arthritis; osteoporosis; inflammation;

KW osteoarthritic; antirheumatic; osteopathic; antiinflammatory;

KW musculoskeletal disease; immune disorder; inflammation; degeneration;

KW endocrine disease; light chain.

XX XX

OS Homo sapiens.

XX XX

PH Key Location/Qualifiers

FT Region 45..56

FT /label= L-CDR1

FT Region 72..76

FT /label= L-CDR2

FT Region 111..119

FT /label= L-CDR3

XX XX

PN WO2006013107-A1.

XX XX

PD 09-FEB-2006.

XX XX

PF 04-AUG-2005; 2005WO-EP008470.

XX XX

PR 05-AUG-2004; 2004GB-00017487.

XX XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

XX XX

PI Di Padova FE, Gram H, Hofstetter H, Jeschke M, Rondeau J;

PI Van Den Berg W;

XX XX

DR WPI; 2006-145760/15.

XX XX

PT Novel interleukin-17 binding molecule capable of inhibiting human IL-17

PT activity and IL-6 production induced by human-IL-17 in human dermal

PT fibroblasts, useful for treating IL-mediated diseases e.g.

PT osteoarthritis.

XX XX

PS Example 3; Page 43-44; 76pp; English.

XX XX

CC The present invention relates to interleukin-17 (IL-17) antagonistic

CC antibodies suitable for use in the treatment of IL-17 mediated diseases

CC and disorders. A claimed IL-17 binding molecule is capable of inhibiting

CC the activity of 1 nM human IL-17 at a concentration of less than 5 nM by

CC 50%, the activity being measured on interleukin-6 production induced by

CC human IL-17 in human dermal fibroblasts. The IL-17 binding molecule

CC comprises: a heavy chain variable region (VH) comprising complementarity

CC determining regions CDR1, CDR2 and CDR3 AEF73686-AEF73688 or CDR1-x, CDR2

CC -x and CDR3-x AEF73696-AEF73698 from anti-human IL-17 antibody AIN457;

CC and a light chain variable region (LH) comprising CDR1', CDR2' and CDR3'

CC AEF73689-AEF73691 from AIN457. The IL-17 binding molecule is preferably a

CC human antibody. It preferably comprises at least one antigen binding site

CC comprising a first domain having amino acid sequence homology to the

CC AIN457 VH region AEF73693 and a second domain having amino acid sequence

CC homology to the AIN457 VL region AEF73695. Also provided are a DNA

CC construct encoding the IL-17 binding molecules of the invention, an

CC expression vector comprising the DNA construct, and a method of producing

CC an IL-17 binding molecule by culturing a transformed host cell line. The

CC IL-17 binding molecule is used to manufacture a medicament for the

CC treatment of an IL-17 mediated disease or disorder, especially

CC osteoarthritis, rheumatoid arthritis, osteoporosis and other inflammatory

CC arthritides. In an example from the invention, transgenic mouse 27340,

CC which is engineered to express the human IgG/kappa repertoire instead of

CC the murine immunoglobulin repertoire, was used to generate antibodies to

CC human IL-17. B-cells from these mice were immortalized by standard

CC hybridoma technology and murine hybridoma cells were obtained which

CC secreted the human IgG1/kappa antibody AIN457. The present sequence is

XX the amino acid sequence of AIN457 VL.

XX XX

CC the amino acid sequence of AIN457 light chain.
 XX Sequence 236 AA;
 SQ

Query Match 97.3%; Score 543; DB 10; Length 236;
 Best Local Similarity 96.3%; Pred. No. 1.3e-33;
 Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
 Db 22 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYATSSRATGIP 81
 Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
 Db 82 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 129

RESULT 8
 ADY26769
 ID ADY26769 standard; protein; 108 AA.
 AC ADY26769;
 XX
 XX 19-MAY-2005 (first entry)
 DT
 XX Anti-NGF-antibody light chain variable region SEQ ID NO 84.
 DE
 XX analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
 KW neurological disease; NGF; nerve growth factor;
 KW light chain variable region.
 KW
 XX Homo sapiens.
 OS
 XX
 XX
 XX PN WO2005019266-A2.
 XX PD 03-MAR-2005.
 XX
 XX 15-JUL-2004; 2004WO-US022876.
 XX
 XX 15-JUL-2003; 2003US-0487431P.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
 PI
 XX WPI; 2005-202606/21.
 DR
 XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful
 PT for manufacturing a medicament for treating painful disorders (e.g. acute
 PT pain) or conditions associated with increased expression or sensitivity
 PT to NGF.
 XX
 XX Claim 33; SEQ ID NO 84; 190pp; English.
 PS
 XX The invention describes an isolated human antibody that interacts with or
 CC binds specifically to human nerve growth factor (NGF) and neutralize the
 CC function of NGF. Also described are: methods of treating a condition
 CC caused by increased expression of NGF or increased sensitivity to NGF in
 CC a patient; methods for detecting NGF in a biological sample; an NGF
 CC specific binding agent comprising any of the 59 amino acid sequences
 CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
 CC specification, and where the binding agent can bind to NGF; a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of the antibody or binding agent cited above; or a
 CC medicament for treating a painful disorder or condition associated with
 CC increased expression of NGF or increased sensitivity to NGF, the
 CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
 CC its immunologically functional immunoglobulin fragment, or pharmaceutical
 CC salts of the monoclonal antibody or the fragment, where the monoclonal
 CC antibody is at least one of the monoclonal antibody cited above, and a
 CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
 CC polynucleotide that encodes the above antibody or binding agent; an
 CC isolated cell line that produces the above antibody or binding agent; an

CC expression vector comprising the above polynucleotide; and a host cell
 CC comprising the nucleic acid or expression vector. The composition
 CC (including the antibody) and methods are useful for manufacturing a
 CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
 CC or pain from trauma or cancer), or a condition associated with increased
 CC expression of NGF or increased sensitivity to NGF. This is the amino acid
 CC sequence of a human NGF antibody light chain variable region.
 XX
 SQ Sequence 108 AA;
 Query Match 95.9%; Score 535; DB 9; Length 108;
 Best Local Similarity 96.3%; Pred. No. 2.6e-33;
 Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
 Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
 Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108

RESULT 9
 ADY26816
 ID ADY26816 standard; protein; 108 AA.
 XX
 AC ADY26816;
 XX
 XX 19-MAY-2005 (first entry)
 DT
 XX Human anti-NGF-antibody light chain SEQ ID NO 131.
 DE
 XX analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
 KW neurological disease; NGF; nerve growth factor; light chain.
 KW
 XX Homo sapiens.
 OS
 XX
 XX PN WO2005019266-A2.
 XX PD 03-MAR-2005.
 XX
 XX 15-JUL-2004; 2004WO-US022876.
 XX
 XX 15-JUL-2003; 2003US-0487431P.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
 PI
 XX WPI; 2005-202606/21.
 DR
 XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful
 PT for manufacturing a medicament for treating painful disorders (e.g. acute
 PT pain) or conditions associated with increased expression or sensitivity
 PT to NGF.
 XX
 XX Claim 33; SEQ ID NO 131; 190pp; English.
 PS
 XX The invention describes an isolated human antibody that interacts with or
 CC binds specifically to human nerve growth factor (NGF) and neutralize the
 CC function of NGF. Also described are: methods of treating a condition
 CC caused by increased expression of NGF or increased sensitivity to NGF in
 CC a patient; methods for detecting NGF in a biological sample; an NGF
 CC specific binding agent comprising any of the 59 amino acid sequences
 CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
 CC specification, and where the binding agent can bind to NGF; a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of the antibody or binding agent cited above; or a
 CC medicament for treating a painful disorder or condition associated with
 CC increased expression of NGF or increased sensitivity to NGF, the
 CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
 CC its immunologically functional immunoglobulin fragment, or pharmaceutical

CC salts of the monoclonal antibody or the fragment, where the monoclonal
 CC antibody is at least one of the monoclonal antibody cited above, and a
 CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
 CC polynucleotide that encodes the above antibody or binding agent; an
 CC isolated cell line that produces the above antibody or binding agent; an
 CC expression vector comprising the above polynucleotide; and a host cell
 CC comprising the nucleic acid or expression vector. The composition
 CC (including the antibody) and methods are useful for manufacturing a
 CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
 CC or pain from trauma or cancer), or a condition associated with increased
 CC expression of NGF or increased sensitivity to NGF. This is the amino acid
 CC sequence of a human NGF antibody light chain.

XX Sequence 108 AA;

Query Match 95.9%; Score 535; DB 9; Length 108;

Best Local Similarity 96.3%; Pred. No. 2.6e-33;

Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

DB 1 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPSCSFQGGTKLEIK 108

DB 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 108

RESULT 10

ID ADZ57709 standard; protein; 128 AA.

XX ADZ57709;

XX 30-JUN-2005 (first entry)

XX Germline antibody A27Vk3, Jk2 light chain protein.

XX antibody engineering; cytostatic; vulnary; vasotropic; cardiant;

XX monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;

XX gastrointestinal ulcer; ischemia; transplant rejection;

XX myocardial infarction; reperfusion injury; restenosis; angioplasty;

XX vascular disease; cancer; retinopathy; endometriosis; arthritis;

XX Alzheimer's disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;

XX antibody.

XX Homo sapiens.

XX GB2404660-A.

XX 09-FEB-2005.

XX 04-AUG-2004; 2004GB-00017384.

XX 04-AUG-2003; 2003US-0492432P.

XX (PFIZ) PFIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL;

XX Jia X;

XX WPI; 2005-145169/16.

XX Human monoclonal antibody or antigen-binding portion that specifically

XX binds to c-Met, useful for treating cancer by inhibiting c-Met or for

XX promoting tissue regeneration and wound healing by activating c-Met.

XX Example 2; SEQ ID NO 18; 128pp; English.

XX The invention relates to a human monoclonal antibody (I) or its antigen-

XX binding portion that specifically binds to c-Met, comprises a heavy chain

XX having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is

CC lysine and X4 is threonine, and a light chain having a fully defined
 CC sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both
 CC chains are without a signal sequence. All the sequences are fully defined
 CC in the specification. (I) is useful for the manufacture of a medicament
 CC for treating a hyperproliferative disorder in a subject, where the
 CC antibody or its portion is a c-Met antagonist. (I) is useful for
 CC manufacture of a medicament for promoting wound healing or tissue
 CC regeneration in a subject, where the antibody, antigen-binding portion or
 CC the composition activates c-Met. (I) which has a c-Met agonist activity
 CC is useful in tissue regeneration or wound healing (skin ulcers or gastric
 CC ulcers), or treating ischemia associated with kidney transplant
 CC rejection, for attenuating toxicity associated with cyclosporin treatment
 CC after transplant surgery, for treating myocardial infarction, cardiac
 CC ischemia due to reperfusion injury, restenosis after angioplasty or
 CC vascular diseases (I) which has a c-Met antagonist activity is useful
 CC for treating cancers of brain, lung, squamous cell, bladder, neck, liver,
 CC prostate, etc., proliferative vitreoretinopathy, proliferative diabetic
 CC retinopathy, endometriosis, and arthritis, for inhibiting plaque
 CC formation in Alzheimer's disease, inhibiting cellular mitogenic
 CC responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas.
 CC (I) is useful for detecting c-Met in a biological sample in vitro or in
 CC vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has
 CC selectivity for c-Met that is at least 100 times greater than their
 CC selectivity for insulin like growth factor I receptor. This sequence
 CC corresponds to the amino acid sequence for a germline antibody light
 CC chain used in the invention.

XX Sequence 128 AA;

Query Match 95.9%; Score 535; DB 9; Length 128;

Best Local Similarity 96.3%; Pred. No. 3e-33;

Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

DB 21 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPSCSFQGGTKLEIK 108

DB 81 DRFSGSGGTDTLTISRLEPEDFAVYCCQYGGSPYTFGGTKLEIK 128

RESULT 11

ID AAR38672 standard; protein; 129 AA.

XX AAR38672;

XX 25-MAR-2003 (revised)

XX 01-NOV-1993 (first entry)

XX vk325-Jk2.

XX Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS; CD4;

XX receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain;

XX epitope; immune deficiency.

XX Homo sapiens.

XX Key

XX Region

XX Peptide

XX Misc-difference 1

XX Protein

XX Misc-difference 35

XX Region

XX Region

XX Location/Qualifiers

XX 1..116

XX /label= vk325

XX 1..20

XX /label= sig_peptide

XX /note= "Met encoded by ATC (sic) "

XX 21..129

XX /label= mat_protein

XX /note= "Pro encoded by GCA (sic) "

XX 44..55

XX /label= CDR1

XX 71..77

multiple sclerosis; neuroprotective; neurological disease;
myasthenia gravis; muscular-gen.; neuroprotective; Crohn's disease;
antifungal; gastrointestinal-gen.; nephritis; nephrotropic;
genitourinary disease; primary biliary cirrhosis; hepatotropic;
pancreatitis; allergy; antiallergic; contact dermatitis; dermatological;
delayed hypersensitivity; inflammatory bowel disease; septic shock;
antibacterial; infection; osteoporosis; osteopathic; degeneration;
endocrine disease; musculoskeletal disease; osteoarthritis;
antiarthritic; osteopathic; musculoskeletal disease; cognitive disorder;
neuropathic; hereditary hemorrhagic telangiectasia; vasotropic; restenosis;
fungal infection; fungicide; parasitic infection; antiparasitic;
viral infection; cytomegalovirus infection; virucide.

Homo sapiens.

WO2006055809-A2.

26-MAY-2006.

18-NOV-2005; 2005WO-US041904.

18-NOV-2004; 2004US-0628815P.

(IMCL-) IMCLONE SYSTEMS INC.

Wu Y, Hicklin DJ, Bohlen P;

WPI; 2006-373517/38.

N-PSDB; AEH89260.

New isolated human monoclonal antibody that binds specifically to
vascular endothelial growth factor receptor-1 for treating cancers and
angiogenic-related disorders, e.g. atherosclerosis.

Claim 6; SEQ ID NO 15; 82pp; English.

The invention relates to an isolated human monoclonal antibody or
fragment that binds specifically to vascular endothelial growth factor
receptor-1 (VEGFR-1) and comprises a light chain complementarity
determining region-2 (CDR2) of 7 amino acids (SEQ ID NO: 2; see AEH89240)
and a light chain CDR3 of 9 amino acids (SEQ ID NO: 3; see AEH89241). Also
included are: an isolated polynucleotide comprising a nucleotide sequence
encoding the antibody or its fragment; an isolated polynucleotide
comprising a nucleotide sequence selected from (AEH89259 to AEH89265),
the nucleotide sequence encoding an antibody or its fragment that
specifically binds to VEGFR-1; an expression vector comprising the
polynucleotide sequence linked to an expression sequence; a recombinant
host cell comprising the expression vector; a method of producing an
antibody or its fragment; a method of modulating activity of VEGFR-1 in a
mammal; a method of inhibiting angiogenesis in a mammal; and a method of
reducing tumor growth in a mammal. The antibody is used to inhibit
angiogenesis and reduce tumor growth in a mammal. The monoclonal
antibodies, polynucleotides, and methods are useful for treating
angiogenic-related disorders (e.g. atherosclerosis, rheumatoid arthritis,
neovascular glaucoma, proliferative retinopathy including proliferative
diabetic retinopathy, macular degeneration, hemangiomas, angiofibromas,
psoriasis, retinopathy of prematurity (retrolental fibroplastic), corneal
graft rejection, insulin-dependent diabetes mellitus, multiple sclerosis,
myasthenia gravis, Crohn's disease, autoimmune nephritis, primary biliary
cirrhosis, acute pancreatitis, allograft rejection, allergic inflammation
(allergic reaction), contact dermatitis and delayed hypersensitivity
reactions, inflammatory bowel disease, septic shock, osteoporosis,
osteoarthritis, cognitive defects induced by neuronal inflammation, Osler
-Weber syndrome (hereditary hemorrhagic telangiectasia), restenosis, and
fungal, parasitic and viral infections, including cytomegaloviral
infections). The present sequence represents anti-VEGFR-1 antibody light
chain variable region SEQ ID NO:15.

Sequence 120 AA;

Query Match 95.5%; Score 533; DB 10; Length 120;

Best Local Similarity 95.4%; Pred. No. 4e-33;

Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRPSGSGGTDFTLTISRLEPEDFAVYVCOQYSGSSPCSGQGTGLEIK 108
DB 61 DRPSGSGGTDFTLTISRLEPEDFAVYVCOQYSGSSPLTFGQGTGLEIK 108

RESULT 14

ID ABJ36930

ABJ36930 standard; protein; 130 AA.

AC ABJ36930;

DT 01-MAY-2003 (first entry)

DE Anti-CD40 monoclonal antibody related protein SEQ ID No 46.

KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
immunoadjuvant; anti-tumour agent; immunosuppressant; allergy;
autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.

OS Unidentified.

XX WO200288186-A1.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-JP004292.

XX 27-APR-2001; 2001WO-US013672.

XX 11-MAY-2001; 2001JP-00142482.

XX 05-OCT-2001; 2001JP-00310535.

XX 26-OCT-2001; 2001US-00040244.

XX (KIRI) KIRIN BEER KK.

XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;

XX WPI; 2003-120463/11.

XX N-PSDB; ABT31872.

XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
or functional fragment, is useful in the treatment of e.g. autoimmune
diseases or cancer.

XX Claim 25; Page 51; 94pp; Japanese.

The invention relates to an antibody to human CD40, or its functional
fragment, has at least one of the following properties: acting on
dendritic cells to produce IL-12 in the presence of LPS
(lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
cells to activate maturity of the dendritic cells with high G28-5
antibody; and activating CD95 expression with high G28-5 antibody against
B cell line. Such antibodies or functional fragments can be used as
immunoadjuvants, anti-tumour agents, immunosuppressants, and as remedies
for autoimmune diseases, allergy or coagulation factor VIII inhibitors
syndrome. This sequence represents a protein relating to the anti-CD40
monoclonal antibody of the invention

XX Sequence 130 AA;

Query Match 95.5%; Score 533; DB 6; Length 130;

Best Local Similarity 95.4%; Pred. No. 4.3e-33;

Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60

DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 80

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPCSFQGGTKLEIK 108
Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPITFGQGRLEIK 128

RESULT 15

AE95253
ID AEG95253 standard; protein; 130 AA.

XX AC AEG95253;

XX DT 01-JUN-2006 (first entry)

DE DE Human immunoglobulin G4 (IgG4) antibody related protein SEQ ID NO 8.
XX immunosuppressive; antiinflammatory; gastrointestinal-gen.; antitumor;
KW dermatological; hemostatic; neuroprotective; antipsoriatic;
KW antirheumatic; cytostatic; antiarteriosclerotic; nephrotropic;
KW immunostimulator; immunoglobulin; IgG4; transplant rejection;
KW immune disorder; systemic lupus erythematosus; dermatological disease;
KW metabolic disorder; musculoskeletal disease;
KW idiopathic thrombocytopenic purpura; genetic disorder;
KW hematological disease; neurological disease; multiple sclerosis;
KW psoriasis; dermatological disease; rheumatism; inflammation; cancer;
KW neoplasm; arteriosclerosis; cardiovascular disease; nephritis;
KW genitourinary disease; Alzheimers disease; degeneration; amyloidosis.

XX OS Homo sapiens.

XX PN WO2006033386-A1.

XX PD 30-MAR-2006.

XX PF 22-SEP-2005; 2005WO-JP017463.

XX PR 22-SEP-2004; 2004JP-00275908.

XX PA (KIRI) KIRIN BEER KK.

XX PI Takahashi N, Yoshida H;

XX DR WPI; 2006-316320/33.

XX DR N-PSDB; AEG95252.

XX PT Novel anti-CD40 antibody having heavy chain constant region of human
PT immunoglobulin G4 including substitution of arginine at specific position
PT by lysine, threonine, methionine or leucine, useful in treating autoimmune
PT disease and cancer.

XX PS Example 1; SEQ ID NO 8; 47pp; Japanese.

XX The invention relates to an antibody comprising heavy chain constant
CC region of human immunoglobulin G4 (IgG4). The antibody being anti-CD40
CC antibody is useful as therapeutic agent of transplant rejection.
CC autoimmune disease, cancer, arteriosclerosis, nephritis, Alzheimer's
CC disease or amyloidosis. The antibody is useful for treating transplant
CC rejection, autoimmune disease (e.g. inflammatory bowel disease, Crohn's
CC disease and ulcerative colitis), systemic lupus erythematosus (SLE),
CC idiopathic thrombocytopenic purpura (ITP) multiple sclerosis, psoriasis,
CC rheumatism, cancer (e.g. lung cancer, colon cancer, rectal cancer, breast
CC pancreatic cancer, liver cancer, prostatic cancer, bladder cancer, breast
CC cancer and stomach cancer), arteriosclerosis, nephritis, Alzheimer's
CC disease and amyloidosis. The antibody exhibits suppressed aggregation
CC formation, and is highly stable mutant of IgG4 antibody. The antibody
CC exhibits decreased aggregate formation in low pH, and maintains binding
CC property with respect to the antigen, thus the side effects caused by
CC aggregate of the antibody can be avoided. The antibody has improved or
CC controlled antibody dependent cell-mediated cytotoxicity and/or
CC complement dependent cytotoxicity. The present sequence represents a
CC human immunoglobulin G4 (IgG4) antibody related protein. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ

Sequence 130 AA;

Query Match 95.5%; Score 533; DB 10; Length 130;
Best Local Similarity 95.4%; Pred. No. 4.3e-33;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 80
QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPCSFQGGTKLEIK 108
Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSSPITFGQGRLEIK 128

Search completed: April 25, 2007, 04:05:22
Job time : 94.661 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 8 Seconds
(without alignments)
1261.509 Million cell updates/sec

Title: US-10-665-383-4

Perfect score: 558

Sequence: 1 EIVLTQSPGTLSPGERAT.....CQYGSPPCSFGQGTKLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	95.9	108	2 C30608	Ig kappa chain V-I
2	535	95.9	109	2 H30601	Ig kappa chain V-I
3	534	95.7	109	2 H30601	Ig kappa chain V-I
4	533	95.5	109	2 H30601	Ig kappa chain V-I
5	531	95.2	109	2 PH0963	Ig kappa chain V-I
6	531	95.2	109	2 D30601	Ig kappa chain V-I
7	530	95.0	109	2 C30601	Ig kappa chain V-I
8	530	95.0	129	2 S46369	Ig kappa chain var
9	530	94.8	134	2 S38643	Ig kappa chain V-I
10	529	94.8	109	2 S30601	Ig kappa chain V-I
11	529	94.8	129	2 S49532	anti-Sm antibody V
12	528	94.6	129	1 K3HUHA	Ig kappa chain pre
13	527	94.4	128	2 S20636	Ig kappa chain V-I
14	526	94.3	129	1 K3HUTI	Ig kappa chain pre
15	524	93.9	109	1 K3HUTI	Ig kappa chain V-I
16	524	93.9	109	2 F30607	Ig kappa chain V-I
17	523.5	93.8	114	2 S46375	Ig kappa chain V-I
18	521	93.4	109	1 K3HUSI	Ig kappa chain V-I
19	520	93.2	109	2 A30608	Ig kappa chain V-I
20	515	92.3	109	2 G30607	Ig kappa chain V-I
21	514	92.1	107	2 PH0965	Ig kappa chain V-I
22	514	92.1	108	2 B30608	Ig kappa chain V-I
23	513	91.9	124	2 S20633	Ig kappa chain - h
24	511	91.6	121	2 S40327	Ig kappa chain - h
25	508	91.0	109	1 K3HULW	Ig kappa chain V-I
26	507	90.9	110	2 S20635	Ig kappa chain V-I
27	504.5	90.4	108	2 E30609	Ig kappa chain V-I
28	503.5	90.2	110	2 E30607	Ig kappa chain V-I
29	503	90.1	108	1 K3HUB6	Ig kappa chain V-I

30	502	90.0	109	2 F44151	Ig kappa chain V-I
31	501.5	89.9	108	2 F44151	Ig kappa chain V-I
32	500	89.6	109	1 K3HUGO	Ig kappa chain V-I
33	500	89.6	130	2 S20637	Ig kappa chain V-I
34	499	89.4	129	2 A32274	Ig kappa chain pre
35	497.5	89.2	110	2 S44120	Ig kappa chain V-I
36	495	88.7	109	2 S47181	Ig kappa chain - h
37	488.5	87.5	104	2 PH0964	Ig kappa chain V-I
38	488	87.5	215	2 JE0242	Ig kappa chain - h
39	486.5	87.2	129	2 S40325	Ig kappa chain V-I
40	485	86.9	96	2 A30601	Ig kappa chain V-I
41	484	86.9	116	2 B27594	Ig kappa chain pre
42	484	86.7	215	2 A23746	Ig kappa chain V-I
43	479	85.8	118	2 T03036	Ig light chain - h
44	477	85.5	108	2 S33988	Ig kappa chain V-I
45	475	85.1	116	2 C27594	Ig kappa chain pre

ALIGNMENTS

RESULT 1

C30608

Ig kappa chain V-III region (Pie) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004

C;Accession: C30608

R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon

J. Immunol. 142, 3158-3163, 1989

A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies

A;Reference number: A30601; MUID:89215279; PMID:2496160

A;Accession: C30608

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-108 <GON>

A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE3

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 108;

Best Local Similarity 96.3%; Pred. No. 3.8e-38;

Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSVLAITYQKPGQAPRLLIYATSSRATGIP 60

Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSVLAITYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFGSGSGTDFLTISRLEPDAFVYCOQYGSPPCSFGQGTKLEIK 108

Db 61 DRFGSGSGTDFLTISRLEPDAFVYCOQYGSPPCSFGQGTKLEIK 108

RESULT 2

H30601

Ig kappa chain V-III region (Gar and Flo) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000

C;Accession: H30601; E30601

R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon

J. Immunol. 142, 3158-3163, 1989

A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies

A;Reference number: A30601; MUID:89215279; PMID:2496160

A;Accession: H30601

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-109 <GON1>

A;Cross-references: UNIPARC:UPI0000011B930

A;Accession: E30601

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-109 <GON2>

A;Cross-references: UNIPARC:UPI0000011B930

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.9%; Score 535; DB 2; Length 109;
Best Local Similarity 96.3%; Pred. No. 3.8e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108
DB 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPYTFGQGTKEIK 108

RESULT 3

F30601
Ig kappa chain V-III region (Neu) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: F30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotype characterization of the L chains of human IgM autoanti
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: F30601
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
A:Cross-references: UNIPARC:UPI0000176AE6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 534; DB 2; Length 109;
Best Local Similarity 93.5%; Pred. No. 4.6e-38;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108
DB 61 DRFTSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPCTFGQGTKEIK 108

RESULT 4

B30601
Ig kappa chain V-III region (Glo) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: B30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotype characterization of the L chains of human IgM autoanti
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: B30601
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
A:Cross-references: UNIPARC:UPI0000176AE7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.5%; Score 533; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 5.6e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108
DB 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPYTFGQGTKEIK 108

RESULT 5

PH0963
Ig kappa chain V region (36+ CLL-SMI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: PH0963
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0963
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-109 <MAR>

A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176A29
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-91/Domain: immunoglobulin homology <IMM>
F:14-34/Region: complementarity-determining 1
F:35-50/Region: framework 2
F:51-56/Region: complementarity-determining 2
F:57-89/Region: framework 3
F:90-97/Region: complementarity-determining 3

Query Match 95.2%; Score 531; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
QY 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPCSFGQGTKEIK 108
DB 61 DRFSGSGSDTFTLTISRLEPEDFAVYCYQYGGSPYTFGQGTKEIK 108

RESULT 6

D30601
Ig kappa chain V-III region (Cur) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: D30601
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A:Title: Structural and idiotype characterization of the L chains of human IgM autoanti
A:Reference number: A30601; MUID:89215279; PMID:2496160
A:Accession: D30601
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>

A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AE9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.2%; Score 531; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSSPCSFGQGTKEIK 108
 Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSSPRTFGQTKVEIK 108

RESULT 7

C30601
 Ig kappa chain V-III region (Pay) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
 C:Accession: C30601
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soló
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: C30601
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <GON>
 A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AEB
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 109;
 Best Local Similarity 94.4%; Pred. No. 9.9e-38;
 Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSSPCSFGQGTKEIK 108
 Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSPLTFGQTKVEIK 108

RESULT 8

S46369
 IG light chain variable region (VJ) - human
 C:Species: Homo sapiens (man)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S46369
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994
 A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
 A:Reference number: S46369; MUID:94313975; PMID:8039491
 A:Accession: S46369
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-129 <BEN>
 A:Cross-references: UNIPARC:UPI0000176CA5; EMBL:Z27170
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 129;
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 80
 QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSSPCSFGQGTKEIK 108
 Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOYSSPPFPFGQGTKEIK 128

RESULT 9

S38643
 IG kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S38643
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 submitted to the EMBL Data Library, November 1993
 A:Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
 A:Reference number: S38643
 A:Accession: S38643
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-134 <BEN>
 A:Cross-references: UNIPARC:UPI00001165A2; EMBL:Z27170; NID:9415955; PIDN:CAA81694.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;41-116/Domain: immunoglobulin homology <IMM>

Query Match 95.0%; Score 530; DB 2; Length 134;
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 Db 26 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 85
 QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSSPCSFGQGTKEIK 108
 Db 86 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOYSSPPFPFGQGTKEIK 133

RESULT 10

G30601
 IG kappa chain V-III region (Got) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
 C:Accession: G30601
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soló
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: G30601
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <GON>
 A:Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176AEB
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 529; DB 2; Length 109;
 Best Local Similarity 95.4%; Pred. No. 1.2e-37;
 Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYATSSRATGIP 60
 QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOQYSSSPCSFGQGTKEIK 108
 Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYVYCOYSSPPFPFGQGTKEIK 108

RESULT 11

S49532
 anti-Sm antibody VL chain (V kappa 3/J kappa 2) - human
 C:Species: Homo sapiens (man)
 C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000.
 C:Accession: S49532
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S49532
 A:Status: preliminary
 A:Molecule type: mRNA

A;Accession: S20636
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <LEE>
A;Cross-references: UNIPARC:UPI00001163DC; EMBL:Z11894; NID:g33200; PIDN:CAA77948.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 94.4%; Score 527; DB 2; Length 128;
Best Local Similarity 94.4%; Pred. No. 2.1e-37;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCOYGSSPCSFQGCKLEIK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 81 DRFGSGSGTDFTLTISRLEPEDFAVYCCOYGSDPRTFGQGTKVEIK 128
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
K3HUI
Ig kappa chain precursor V-III region (Hic) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: PU0021
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Antibody-associated kappa light chain variable region gene expressed in chro
A;Reference number: PU0021; MUID:88171307; PMID:3127527
A;Accession: PU0021
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
A;Cross-references: UNIPROT:P18136; UNIPARC:UPI000012E164
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed in
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F;21-117/Region: V segment
F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;118-129/Region: J segment (JK1)
F;43-109/Disulfide bonds: #status predicted

Query Match 94.3%; Score 526; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.5e-37;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYATSSRATGIP 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 DRFGSGSGTDFTLTISRLEPEDFAVYCCOYGSSPCSFQGCKLEIK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 81 DRFGSGSGTDFTLTISRLEPDFAVYCCOYGSSPWTFGQGTKVEIK 128
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
K3HUI
Ig kappa chain V-III region (Ti) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text change 09-Jul-2004

C;Accession: A01895
R;Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A;Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91651; MUID:72188439; PMID:5027703
A;Accession: A01895
A;Molecule type: protein
A;Residues: 1-109 <SUT>
A;Cross-references: UNIPROT:P01622; UNIPARC:UPI000012E15D
A;Note: the sequence of the C region, which has the Inv (3) marker, is also given
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-91/Domain: immunoglobulin homology <IMM>
F;23-89/Disulfide bonds: #status predicted

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 3.2e-37;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSVLAWYQKPGQAPRLIIYATSSRATGIP 60
|||||
Db 1 EIVLTQSPGTLSPGERATLSCRSQSVNSFLAWYQKPGQAPRLIIYVASSRATGIP 60
|||||

QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGSSPFCGQTKLEIK 108
|||||
Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYQCQYGSSPFCGQTKVELK 108
|||||

Search completed: April 25, 2007, 04:06:40
Job time : 8.23729 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 74 Seconds
(without alignments)
1574.822 Million cell updates/sec

Title: US-10-665-383-4

Perfect score: 558

Sequence: 1 EIVLTQSPGTLSPERAT.....CQYGGSPGFGQGTKLEIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 8.4:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	94.6	129	1 KV3L HUMAN	P18135 homo sapien
2	526	94.3	129	1 KV3M HUMAN	P18136 homo sapien
3	524	93.9	109	1 KV3D HUMAN	P01622 homo sapien
4	521	93.4	109	1 KV3B HUMAN	P01620 homo sapien
5	518	92.8	109	2 Q9UL78 HUMAN	Q9UL78 homo sapien
6	508	91.0	209	1 KV3E HUMAN	P01623 homo sapien
7	506.5	90.8	236	2 Q6PIL8 HUMAN	Q6PIL8 homo sapien
8	504	90.3	109	2 Q9UL86 HUMAN	Q9UL86 homo sapien
9	503	90.1	108	1 KV3A HUMAN	P01619 homo sapien
10	500	89.6	109	1 KV3G HUMAN	P04206 homo sapien
11	493	88.4	235	2 Q6PJF2 HUMAN	Q6PJF2 homo sapien
12	491	88.0	235	2 Q6GMV9 HUMAN	Q6GMV9 homo sapien
13	481.5	86.3	236	2 Q6P5S8 HUMAN	Q6P5S8 homo sapien
14	466	83.5	100	1 KV3C HUMAN	P01621 homo sapien
15	465.5	83.4	128	1 KV3K HUMAN	P06311 homo sapien
16	446	79.9	109	1 KV3F HUMAN	P01624 homo sapien
17	445.5	79.8	234	2 Q5G9I9 HUMAN	Q5G9I9 homo sapien
18	439	78.7	129	1 KV3H HUMAN	P04207 homo sapien
19	435.5	78.0	108	2 Q9UL83 HUMAN	Q9UL83 homo sapien
20	426	76.3	109	2 Q9UL85 HUMAN	Q9UL85 homo sapien
21	420.5	75.4	115	1 KV3I HUMAN	P04433 homo sapien
22	420	75.3	235	2 Q6GMW0 HUMAN	Q6GMW0 homo sapien
23	415.5	74.5	114	1 KV4A HUMAN	P01625 homo sapien
24	414	74.2	116	1 KV3J HUMAN	P04434 homo sapien
25	399.5	71.6	134	1 KV4C HUMAN	P06314 homo sapien
26	398.5	71.4	108	2 Q9UL79 HUMAN	Q9UL79 homo sapien
27	397.5	71.2	108	1 KV1H HUMAN	P01600 homo sapien
28	394.5	70.7	236	2 Q6PIH7 HUMAN	Q6PIH7 homo sapien
29	390.5	70.0	208	2 Q9UL77 HUMAN	Q9UL77 homo sapien
30	387	69.4	133	1 KV4B HUMAN	P06313 homo sapien
31	386.5	69.3	108	2 Q9UL70 HUMAN	Q9UL70 homo sapien

32	386.5	69.3	236	2 Q6GMX8 HUMAN	Q6GMX8 homo sapien
33	384	68.8	114	2 Q8KIF1 MOUSE	Q8KIF1 mus musculus
34	383.5	68.7	131	2 Q8LIC3 MOUSE	Q8LIC3 mus musculus
35	382.5	68.5	108	1 KV1M HUMAN	P01605 homo sapien
36	382.5	68.5	236	2 Q6GMX9 HUMAN	Q6GMX9 homo sapien
37	382.5	68.5	236	2 Q7Z3Y4 HUMAN	Q7Z3Y4 homo sapien
38	381.5	68.4	244	2 Q6SZC8 HUMAN	Q6SZC8 homo sapien
39	381	68.3	107	2 Q96SA9 HUMAN	Q96SA9 homo sapien
40	380.5	68.2	108	1 KV1F HUMAN	P01598 homo sapien
41	379.5	68.0	108	1 KV1K HUMAN	P01603 homo sapien
42	378.5	67.8	234	2 Q7Z473 HUMAN	Q7Z473 homo sapien
43	377.5	67.7	236	2 Q6PIT5 HUMAN	Q6PIT5 homo sapien
44	377.5	67.7	240	2 Q6SZC9 HUMAN	Q6SZC9 homo sapien
45	376.5	67.5	255	2 Q6KB05 MOUSE	Q6KB05 mus musculus

ALIGNMENTS

RESULT 1
KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 30-MAY-2006, entry version 43.
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
RL -!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
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CC PIR; P18135; K3HUHA.
CC HSSP; P01625; IEEQ.
CC SMR; P18135; 21-129.
CC Ensembl; ENSG00000169769; Homo sapiens.
CC LinkHub; P18135; -
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig-sub.
CC InterPro; IPR013106; Ig V-set.
CC InterPro; IPR003596; Ig_V-set_sub.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT REGION 21 43 /FTid=PRO_0000015179.
FT REGION 44 55 Framework-1.
FT REGION 56 70 Complementarity-determining-1.
FT REGION 71 77 Framework-2.
FT REGION 78 109 Complementarity-determining-2.
FT REGION 110 118 Framework-3.
FT REGION 119 118 Complementarity-determining-3.

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FT REGION 119 129 JKI segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 94.6%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.1e-47;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTKEIK 108
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTKEIK 128

RESULT 2
KV3M HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 30-MAY-2006, entry version 43.
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC PIR; P18021; K3HUH1.
CC HSSP; P01625; 1EE0.
CC SMR; P18136; 21-129.
CC Ensembl; ENSG00000169769; Homo sapiens.
CC LinkHub; P18136; -.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_V-set.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HIC.
FT FTId=PRO_0000015180.
FT
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JKI segment.

FT REGION 119 129 JKI segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 94.6%; Score 528; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 2.1e-47;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTKEIK 108
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTKEIK 128

RESULT 3
KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 44.
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC PIR; A01895; K3HUT1.
CC HSSP; P01622; 1LVE.
CC SMR; P01622; 1-109.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_V-set.
CC InterPro; IPR003596; Ig_V-set_sub.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >109 Ig kappa chain V-III region Ti.
FT FTId=PRO_0000059764.
FT
FT DISULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 93.9%; Score 524; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 4.6e-47;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

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Db      1  EIVLTSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLLIYVASSRATGIP 60
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        |||||
Db      61  DRFGSGSGTDFLTISRLEPEDFVAVYCOQYSSPCSGFGQTKLEIK 108
        |||||

RESULT 4
KV3B_HUMAN  STANDARD;          PRT;   109 AA.
AC  P01620;
DT  21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT  21-JUN-1986, sequence version 1.
DT  30-MAY-2006, entry version 42.
DE  Ig kappa chain V-III region SIE.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC  Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=82046598; PubMed=6794615;
RA  Andrews D.W., Capra J.D.;
RT  "Amino acid sequence of the variable regions of light chains from two
RT  idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT  group.";
RL  Biochemistry 20:5816-5822(1981).
CC  -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC  globulin activity.
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  PIR; A01892; KJHUS1.
DR  HSSP; P01625; 1LVE.
DR  SMR; P01620; 1-109.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003599; Ig sub.
DR  InterPro; IPR013106; Ig_v-set.
DR  InterPro; IPR003596; Ig_v-set_sub.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IG; 1.
DR  PROSITE; PS00835; IG_LIKE; 1.
DR  Direct protein sequencing; Immunoglobulin domain;
KW  Immunoglobulin V region.
FT  CHAIN 1 >109
FT  DISULFID 23 89
FT  NON TER 109 109
FT  SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
SQ  Ig kappa chain V-III region SIE.
      /FTID=PRO_0000059763.
      By similarity.
Query Match 93.4%; Score 521; DB 1; Length 109;
Best Local Similarity 92.6%; Pred. No. 9.6e-47;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1  EIVLTSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLLIYVASSRATGIP 60
        |||||
Db      1  EIVLTSPGTLSPGERATLSCRASQSVNSFLAWYQKPGQAPRLLIYVASSRATGIP 60
        |||||

Qy      61  DRFGSGSGTDFLTISRLEPEDFVAVYCOQYSSPCSGFGQTKLEIK 108
        |||||
Db      61  DRFGSGSGTDFLTISRLEPEDFVAVYCOQYSSPCSGFGQTKLEIK 108
        |||||

RESULT 5
Q9UL78_HUMAN  PRELIMINARY;          PRT;   109 AA.
ID  Q9UL78
AC  Q9UL78;
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DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain.
 FT NON_TER 109 109
 FT SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;
 SQ
 Query Match 92.8%; Score 518; DB 2; Length 109;
 Best Local Similarity 93.5%; Pred. No. 2e-46;
 Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 QY 61 DRFGSGSGTDTLTISRLPEDFAVYVYQQYGGSPCSFGQGTKEIK 108
 DB 61 DRFGSGSGTDTLTISRLPEDFAVYVYQQYGGSPCSFGQGTKEIK 108
 RESULT 6
 KV3E HUMAN STANDARD; PRT; 109 AA.
 AC P01623;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 30-MAY-2006, entry version 42.
 DE Ig kappa chain V-III region WOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 RT group.";
 RL Biochemistry 20:5816-5822(1981).
 CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
 CC globulin activity.
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 CC -----
 DR PIR; A01896; K3HUVL.
 DR HSP; P01625; LLVE.
 DR SMR; P01623; 1-109.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0008955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT CHAIN 1 >109 Ig kappa chain V-III region WOL.
 FT DISULFID 23 89 /FTIDEPRO_0000059765.
 FT NON_TER 109 109 By similarity.
 FT SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;
 SQ
 Query Match 91.0%; Score 508; DB 1; Length 109;
 Best Local Similarity 91.7%; Pred. No. 2.2e-45;

Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 QY 61 DRFGSGSGTDTLTISRLPEDFAVYVYQQYGGSPCSFGQGTKEIK 108
 DB 61 DRFGSGSGTDTLTISRLPEDFAVYVYQQYGGSPCSFGQGTKEIK 108
 RESULT 7
 Q6PIL8 HUMAN PRELIMINARY; PRT; 236 AA.
 ID O6PIL8_HUMAN
 AC O6PIL8;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 27-JUN-2006, entry version 20.
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
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 CC -----
 DR EMBL; BC032451; AAH32451.1; -; mRNA.
 DR HSP; P01837; 1KCU.
 DR SMR; P01837; 21-236.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1-set.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.

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DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match          90.8%; Score 506.5; DB 2; Length 236;
Best Local Similarity 90.8%; Pred. No. 8.1e-45;
Matches 99; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
DB 21 ENVTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108
DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 129

RESULT 8
ID Q9UL86 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
CC -----
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CC -----
DR EMBL; AF035028; AAD56264.1; -; mRNA.
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSSP; P01625; 1EK3.
DR SMR; Q9UL86; 1-109.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Query Match          90.3%; Score 504; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 5.9e-45;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
DB 21 ENVTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108
DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 129

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Db 1 EIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
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DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108

RESULT 9
ID KV3A HUMAN STANDARD; PRT; 108 AA.
AC P01619;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 40.
DE Ig kappa chain V-III region B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP PROTEIN SEQUENCE.
RX PubMed=11946339; DOI=10.1016/0014-5793(69)80048-7;
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6.";
RL FEBS Lett. 2:301-304 (1969).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC -----
DR PIR; A01891; K3HUB6.
DR HSSP; P01625; 1EEQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >108
FT DISULFID 23 89
FT NON TER 108 108
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11636 MW; 8BC14FF07A419E3D CRC64;

Query Match          90.1%; Score 503; DB 1; Length 108;
Best Local Similarity 86.1%; Pred. No. 7.5e-45;
Matches 93; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

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DB 1 ZIVLTQSPGTLSPGERATLSRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 60
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGSS-PCSFQGTQKLEIK 108

RESULT 10
ID KV3G HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
DT 20-MAR-1987, sequence version 1.
DT 30-MAY-2006, entry version 41.
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
 RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
 RT "Amino acid sequence of a light chain variable region of a human
 RT rheumatoid factor of the Wa idiotype group, in part predicted by its
 RT reactivity with anti-peptide antibodies";
 RL Mol. Immunol. 23:239-244 (1986).
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 CC -----
 DR PIR; A01893; K3HUGO.
 DR HSP; P01625; 1EX3.
 DR SMR; P04206; 1-109.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT CHAIN 1 >109 Ig kappa chain V-III region GOL.
 FT DISULFID 23 89 /FTIDEPRO_0000059767.
 FT NON TER 109 109 By similarity.
 SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;
 Query Match 89.6%; Score 500; DB 1; Length 109;
 Best Local Similarity 89.8%; Pred. No. 1.6e-44;
 Matches 97; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSSVSSYLAWYQQKPGQAPRLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRALSSRYLAWYQQKPGQAPRLIYATSSRATGIP 60
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
 DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
 RESULT 11
 Q6PJF2 HUMAN
 ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.
 AC Q6PJF2
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 27-JUN-2006, entry version 21.
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Shevchenko Y.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC -----
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 CC -----
 DR EMBL; BC016380; AAH16380.1; -; mRNA.
 DR HSP; P01837; 1KCU.
 DR SMR; Q6PJF2; 21-235.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via ...; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1-set.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
 KW Transmembrane.
 SQ SEQUENCE 235 AA; 25521 MW; F33A145A396BA285 CRC64;
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 Best Local Similarity 88.0%; Pred. No. 2.1e-43;
 Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
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 DB 21 EIVLTQSPATLSGPGSRATLSCRAIQIVSAVLAWYQQKPGQAPRLIMFSSSRATGIP 80
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTKEIK 108
 DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSGTGGTGVKDIK 128
 RESULT 12
 Q6GMV9 HUMAN
 ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.
 AC Q6GMV9
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 27-JUN-2006, entry version 21.
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;
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 Best Local Similarity 85.3%; Pred. No. 3.5e-42;
 Matches 93; Conservative 9; Mismatches 6; Indels 1; Gaps 1;
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 QY 61 DRFSGSGSTDTLTISRLEPEDFAVYCCQYGSSP-CSFGQGTKEIK 108
 DB 81 DRFSGSGSTDTLTISRLEPEDFAVYCCQYGTSPLTGGGTRVEIK 129
 RESULT 14
 KV3C_HUMAN STANDARD; PRT; 100 AA.
 AC P01621;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 30-MAY-2006, entry version 44.
 DE Ig kappa chain V-III region NG9 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=84093600; PubMed=6419127; DOI=10.1038/307077a0;
 RA Bentley D.L.;
 RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
 RT a small family of germ-line V genes.";
 RL Nature 307:77-80(1984).
 CC -!- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.
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 DR PIR; A01894; K3HUNG.
 DR HSSP; P01625; 1EEQ.
 DR SMR; P01621; 5-99.
 DR Ensembl; ENSG00000169769; Homo sapiens.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig sub.
 DR InterPro; IPR013106; Ig_v-set.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
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 AC P06311;
 DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
 DT 01-JAN-1988, sequence version 1.
 DT 30-MAY-2006, entry version 44.
 DE Ig kappa chain V-III region IARC/BL41 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=86041852; PubMed=2997711;
 RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 RT III.";
 RL Nucleic Acids Res. 13:6499-6513(1985).
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 CC -----
 DR EMBL; Z00021; CAA77316.1; -; Genomic DNA.
 DR PIR; A01899; K3HU41.
 DR HSSP; P01625; 1EEQ.
 DR SMR; P06311; 21-128.
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 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig sub.
 DR InterPro; IPR013106; Ig_v-set.
 DR InterPro; IPR003596; Ig_v-set_sub.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 128
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 FT /FTID=PRO_0000015178.
 FT Framework-1.
 FT Complementarity-determining-1.
 FT Framework-2.
 FT Complementarity-determining-2.
 FT Framework-3.
 FT Complementarity-determining-3.
 FT REGION 109 117
 FT REGION 118 128
 FT REGION 118 128
 FT DISULFID 43 108
 FT NON_TER 128 128
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 Query Match 83.4%; Score 465.5; DB 1; Length 128;
 Best Local Similarity 87.0%; Pred. No. 8.1e-41;
 Matches 94; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
 QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 60
 DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPKGAPRLLIYATSSRATGIP 79
 QY 61 DRFSGSGSTDTLTISRLEPEDFAVYCCQYGSSP-CSFGQGTKEIK 108
 DB 80 DRFSGSGSTDTLTISRLEPEDFAVYCCQYSTPYTGGTKEIK 127
 Search completed: April 25, 2007, 04:06:37
 Job time : 73.5254 secs

Result No.	Score			DB	ID	Description
	94	Match	%			
1	530	95.0	108	1	US-08-232-081B-42	Sequence 42, Appl
2	529	94.8	109	2	US-09-025-769B-16	Sequence 16, Appl
3	529	94.8	109	2	US-09-490-070A-16	Sequence 16, Appl
4	529	94.8	109	2	US-09-490-153-16	Sequence 16, Appl
5	529	94.8	109	2	US-09-490-324-16	Sequence 16, Appl
6	528	94.6	108	2	US-09-644-668A-9	Sequence 9, Appl
7	525	94.1	108	1	US-08-488-113B-150	Sequence 150, App
8	525	94.1	108	1	US-08-477-484B-150	Sequence 150, App
9	525	94.1	108	1	US-08-646-360-150	Sequence 150, App
10	525	94.1	108	2	US-08-839-765-150	Sequence 150, App
11	525	94.1	108	2	US-09-136-389-150	Sequence 150, App
12	525	94.1	108	2	US-09-610-838-150	Sequence 150, App
13	525	94.1	108	2	US-09-711-485-150	Sequence 150, App
14	524.5	94.0	226	2	US-09-456-090A-50	Sequence 50, Appl
15	524.5	94.0	226	2	US-09-456-090A-86	Sequence 86, Appl
16	524.5	94.0	226	2	US-09-453-234-50	Sequence 50, Appl
17	524.5	94.0	226	2	US-09-453-234-86	Sequence 86, Appl
18	522	93.5	108	2	US-09-644-668A-7	Sequence 7, Appl
19	521	93.4	235	2	US-09-472-087-14	Sequence 14, Appl
20	521	93.4	235	2	US-09-472-087-65	Sequence 65, Appl
21	518.5	92.9	226	2	US-09-456-030A-80	Sequence 80, Appl
22	518.5	92.9	226	2	US-09-453-234-80	Sequence 80, Appl
23	518.5	92.9	236	2	US-09-850-053-34	Sequence 34, Appl
24	518	92.8	108	2	US-09-240-274-178	Sequence 178, App
25	518	92.8	108	2	US-09-848-798-178	Sequence 178, App
26	513.5	92.0	236	2	US-09-850-053-38	Sequence 38, Appl

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Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQORPGQAPRLIIYGASSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPSCSPGQGTGLEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPFLTFGQGTKEIK 108

RESULT 2
US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-16

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 94.4%; Pred. No. 28-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQORPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQORPGQAPRLIIYGASSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPSCSPGQGTGLEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPFLTFGQGTKEIK 108

RESULT 3
US-09-490-070A-16
; Sequence 16, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
```

```
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-490-070A-16

Query Match 94.8%; Score 529; DB 2; Length 109;
Best Local Similarity 94.4%; Pred. No. 28-42;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQORPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQORPGQAPRLIIYGASSRATGIP 60

QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPSCSPGQGTGLEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYQCQYGGSPFLTFGQGTKEIK 108

RESULT 4
US-09-490-153-16
; Sequence 16, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
```

STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-490-153-16

Query Match 94.8%; Score 529; DB 2; Length 109;

Best Local Similarity 94.4%; Pred. No. 2e-42;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108

RESULT 5

US-09-490-324-16

Sequence 16, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-490-324-16

Query Match 94.8%; Score 529; DB 2; Length 109;

Best Local Similarity 94.4%; Pred. No. 2e-42;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108

RESULT 6

US-09-644-668A-9

Sequence 9, Application US/09644668A

Patent No. 6984720

GENERAL INFORMATION:

APPLICANT: Koorman, Alan J.

APPLICANT: Halk, Edward L.

APPLICANT: Lonberg, Nils

APPLICANT: Medarex, Inc.

TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses

FILE REFERENCE: 014643-010510US

CURRENT APPLICATION NUMBER: US/09/644,668A

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/150,452

PRIOR FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 9

LENGTH: 108

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: light chain variable region predicted sequence for

OTHER INFORMATION: 4B6 from V κ A-27

US-09-644-668A-9

Query Match 94.6%; Score 528; DB 2; Length 108;

Best Local Similarity 94.4%; Pred. No. 2.5e-42;

Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSPCSFQGQTKLEIK 108

RESULT 7
US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 4; Indels 0; Gaps 0;
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSFQGTKEIK 108
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSFQGTKEIK 108

RESULT 8
US-08-477-484B-150
; Sequence 150, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-150

Query Match 94.1%; Score 525; DB 1; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSFQGTKEIK 108
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYVYCOQYSSPCSFQGTKEIK 108

RESULT 9

US-08-646-360-150
 ; Sequence 150, Application US/08646360
 ; Patent No. 5837491
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,360
 ; FILING DATE: 13-MAY-1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/05348
 ; FILING DATE: 12-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 200-70.P4
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-646-360-150

Query Match 94.1%; Score 525; DB 1; Length 108;
 Best Local Similarity 94.4%; Pred. No. 4.7e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 QY 61 DRPSSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108
 DB 61 DRPSSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108

RESULT 10

US-08-839-765-150
 ; Sequence 150, Application US/08839765
 ; Patent No. 6146631
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/839,765
 ; FILING DATE: 15-APR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-839-765-150

Query Match 94.1%; Score 525; DB 2; Length 108;
 Best Local Similarity 94.4%; Pred. No. 4.7e-42;
 Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
 QY 61 DRPSSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108
 DB 61 DRPSSGSGTDFLTISRLEPDPFAVYCCQYGSPPCSFGQGTKEIK 108

RESULT 11
 US-09-136-389-150

Sequence 150, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-150

Query Match 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVLTQSPGTLSPGGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EVLTQSPGTLSPGGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSPCSFGQTKLEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSPXPTFGQTKVEIK 108

RESULT 12

US-09-610-838-150
Sequence 150, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-150

Query Match 94.1%; Score 525; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.7e-42;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVLTQSPGTLSPGGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EVLTQSPGTLSPGGERATLSCRSQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
QY 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSPCSFGQTKLEIK 108
DB 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGGSPXPTFGQTKVEIK 108

RESULT 13
 US-09-711-485-150
 ; Sequence 150, Application US/09711485
 ; Patent No. 6649742
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroli, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/711,485
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/839,765
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 150:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-711-485-150
 ;
 ; Query Match 94.1%; Score 525; DB 2; Length 108;
 ; Best Local Similarity 94.4%; Pred. No. 4.7e-42;
 ; Matches 102; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 ;
 QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAHWYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAHWYQKPGQAPRLIIYATSSRATGIP 60
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYSSPCSFQGTGKLEIK 108
 DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYSSPCSFQGTGKLEIK 108

RESULT 14
 US-09-456-090A-50
 ; Sequence 50, Application US/09456090A
 ; Patent No. 6680209
 ; GENERAL INFORMATION:
 ; APPLICANT: Buechler, Joe
 ; APPLICANT: Walkers, Gunars
 ; APPLICANT: Gray, Jeff
 ; APPLICANT: Lonberg, Nils
 ; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
 ; FILE REFERENCE: 020015-000200US
 ; CURRENT APPLICATION NUMBER: US/09/456,090A
 ; CURRENT FILING DATE: 1999-12-06
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 50
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: M1-23L
 ; US-09-456-090A-50
 ;
 ; Query Match 94.0%; Score 524.5; DB 2; Length 226;
 ; Best Local Similarity 95.4%; Pred. No. 1.2e-41;
 ; Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 ;
 QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAHWYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAHWYQKPGQAPRLIIYATSSRATGIP 60
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYSS-PCSFQGTGKLEIK 108
 DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYSSPPYTFQGTGKLEIK 109
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 RESULT 15
 US-09-456-090A-86
 ; Sequence 86, Application US/09456090A
 ; Patent No. 6680209
 ; GENERAL INFORMATION:
 ; APPLICANT: Buechler, Joe
 ; APPLICANT: Walkers, Gunars
 ; APPLICANT: Gray, Jeff
 ; APPLICANT: Lonberg, Nils
 ; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
 ; FILE REFERENCE: 020015-000200US
 ; CURRENT APPLICATION NUMBER: US/09/456,090A
 ; CURRENT FILING DATE: 1999-12-06
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 86
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: M2-33L
 ; US-09-456-090A-86
 ;
 ; Query Match 94.0%; Score 524.5; DB 2; Length 226;
 ; Best Local Similarity 95.4%; Pred. No. 1.2e-41;
 ; Matches 104; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 ;
 QY 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAHWYQKPGQAPRLIIYATSSRATGIP 60
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSVSSSYLAHWYQKPGQAPRLIIYATSSRATGIP 60
 QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYSS-PCSFQGTGKLEIK 108
 DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOQYSSPPYTFQGTGKLEIK 109
 ;
 Search completed: April 25, 2007, 04:08:33
 Job time : 14.5763 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 40 Seconds
(without alignments)
1251.741 Million cell updates/sec

Title: US-10-665-383-4
Perfect score: 558
Sequence: 1 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	108	4	US-10-041-860-49 Sequence 49, Appl
2	558	100.0	108	4	US-10-041-860-225 Sequence 225, App
3	558	100.0	108	4	US-10-041-860-259 Sequence 259, App
4	558	100.0	108	4	US-10-041-860-375 Sequence 375, App
5	558	100.0	108	4	US-10-665-383-4 Sequence 4, Appl
6	535	95.9	108	5	US-10-891-658-84 Sequence 18, Appl
7	535	95.9	108	5	US-10-910-901-18 Sequence 131, App
8	535	95.9	128	5	US-10-309-762-156 Sequence 156, App
9	533	95.5	130	4	US-10-693-629-46 Sequence 123, App
10	532	95.3	108	4	US-10-307-724-123 Sequence 123, App
11	532	95.3	108	5	US-10-737-290-123 Sequence 123, App
12	532	95.3	109	5	US-10-725-962-27 Sequence 27, Appl
13	532	95.3	120	5	US-10-506-743-2 Sequence 2, Appl
14	532	95.3	130	5	US-10-737-290-161 Sequence 161, App
15	532	95.3	215	4	US-10-307-724-122 Sequence 122, App
16	532	95.3	215	5	US-10-737-290-122 Sequence 122, App
17	532	95.3	239	5	US-10-737-290-142 Sequence 142, App
18	530	95.0	384	4	US-10-291-265-804 Sequence 804, App
19	530	95.0	384	4	US-10-291-265-805 Sequence 805, App
20	530	95.0	384	4	US-10-291-265-806 Sequence 806, App
21	530	95.0	384	4	US-10-291-265-807 Sequence 807, App
22	530	95.0	384	4	US-11-000-463-804 Sequence 804, App
23	530	95.0	384	6	US-11-000-463-804 Sequence 805, App
24	530	95.0	384	6	US-11-000-463-805 Sequence 806, App
25	530	95.0	384	6	US-11-000-463-806 Sequence 807, App
26	530	95.0	384	6	US-11-000-463-807 Sequence 21, Appl
27	529	94.8	108	4	US-10-269-711-21 Sequence 21, Appl

28	529	94.8	108	4	US-10-684-109-21 Sequence 21, Appl
29	529	94.8	109	5	US-10-834-397-16 Sequence 16, Appl
30	528	94.6	108	3	US-09-948-939-9 Sequence 9, Appl
31	528	94.6	108	6	US-11-040-846-9 Sequence 9, Appl
32	528	94.6	247	6	US-11-056-825-8 Sequence 8, Appl
33	528	94.6	249	6	US-11-056-825-4 Sequence 4, Appl
34	526	94.3	108	4	US-10-338-366-4 Sequence 4, Appl
35	526	94.3	108	5	US-10-850-635-6 Sequence 6, Appl
36	526	94.3	109	5	US-10-371-942-112 Sequence 112, App
37	526	94.3	109	5	US-10-726-332-210 Sequence 210, App
38	526	94.3	109	5	US-10-938-353-114 Sequence 114, App
39	526	94.3	235	5	US-10-938-353-60 Sequence 60, Appl
40	525.5	94.2	131	4	US-10-478-056-27 Sequence 27, Appl
41	525.5	94.2	131	5	US-10-721-763-27 Sequence 27, Appl
42	525	94.1	106	4	US-10-309-762-163 Sequence 163, App
43	525	94.1	108	4	US-10-127-890-150 Sequence 150, App
44	525	94.1	108	5	US-10-717-243-150 Sequence 150, App
45	524.5	94.0	109	4	US-10-073-644C-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-10-041-860-49
; Sequence 49, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-49

Query Match 100.0%; Score 558; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 5e+40;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 60
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Db 1 EIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQOKPGQAPRLLIYATSSRATGIP 60
|||||

QY 61 DRFGSGSGGDTFTLTISRLEPEDFVAVYCOQYSSPCSGQGTKEIK 108
|||||

Db 61 DRFGSGSGGDTFTLTISRLEPEDFVAVYCOQYSSPCSGQGTKEIK 108
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RESULT 2

US-10-041-860-225
; Sequence 225, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi

; Sequence 84, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 108
; TYPE: PR1
; ORGANISM: homo sapien
US-10-891-658-84

Query Match 95.9%; Score 535; DB 5; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.5e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYVASSRATGIP 60
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGQGTLEIK 108

RESULT 7
US-10-891-658-131
; Sequence 131, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131
; LENGTH: 108
; TYPE: PR1
; ORGANISM: homo sapien
US-10-891-658-131

Query Match 95.9%; Score 535; DB 5; Length 108;
Best Local Similarity 96.3%; Pred. No. 4.5e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYGASSRATGIP 60
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108

Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGQGTLEIK 108
RESULT 8
US-10-910-901-18
; Sequence 18, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO c-MET
; FILE REFERENCE: AEX-PP5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 128
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-910-901-18

Query Match 95.9%; Score 535; DB 5; Length 128;
Best Local Similarity 96.3%; Pred. No. 5.4e-38;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYATSSRATGIP 60
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYGASSRATGIP 80
QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 81 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGQGTLEIK 128

RESULT 9
US-10-309-762-156
; Sequence 156, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 108
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-309-762-156

Query Match 95.5%; Score 533; DB 4; Length 108;
Best Local Similarity 95.4%; Pred. No. 6.7e-36;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLIIYATSSRATGIP 60
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QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPCSFGQGTLEIK 108
DB 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGGSPYTFGQGTLEIK 108

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; OTHER INFORMATION: antibody light chain variable region
US-10-307-724-123

Query Match          95.3%; Score 532; DB 4; Length 108;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||

RESULT 12
US-10-737-290-123
; Sequence 123, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orenicia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain variable region
US-10-737-290-123

Query Match          95.3%; Score 532; DB 5; Length 108;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||

RESULT 13
US-10-725-962-27
; Sequence 27, Application US/10725962
; Publication No. US20050013809A1
; GENERAL INFORMATION:
; APPLICANT: Samuel M. Owens
; APPLICANT: Frank I. Carroll
; APPLICANT: Philip Abraham
; APPLICANT: Melinda G. Gunnell

```

```

; OTHER INFORMATION: antibody light chain variable region
US-10-307-724-123

Query Match          95.3%; Score 532; DB 4; Length 108;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
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RESULT 12
US-10-737-290-123
; Sequence 123, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orenicia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 123
; LENGTH: 108
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain variable region
US-10-737-290-123

Query Match          95.3%; Score 532; DB 5; Length 108;
Best Local Similarity 95.4%; Pred. No. 8.2e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
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DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVCOQYGSSPCSPGQGTKLBIK 108
   |||||

RESULT 13
US-10-725-962-27
; Sequence 27, Application US/10725962
; Publication No. US20050013809A1
; GENERAL INFORMATION:
; APPLICANT: Samuel M. Owens
; APPLICANT: Frank I. Carroll
; APPLICANT: Philip Abraham
; APPLICANT: Melinda G. Gunnell

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```
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Xiao Feng
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; FILE REFERENCE: ABGENIX.071A
; CURRENT APPLICATION NUMBER: US/10/725,962
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-27

Query Match          95.3%; Score 532; DB 5; Length 109;
Best Local Similarity 95.4%; Pred. No. 8.3e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYQCQYGGSPCSFGQGTKLEIK 108
   |||||
Db 61 DRFSGSGGTDFLTISRLEPEDFAVYQCQYGGSPWTFGQGTKVEIK 108
   |||||

RESULT 14
US-10-506-743-2
; Sequence 2, Application US/10506743
; Publication No. US20050106140A1
; GENERAL INFORMATION:
; APPLICANT: Lancaster, Joanne. Sloan
; TITLE OF INVENTION: Antagonistic Anti-hFas Ligand Human Antibodies and Fragments
; FILE REFERENCE: X15450 - National Stage
; CURRENT APPLICATION NUMBER: US/10/506,743
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/367,054
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-743-2

Query Match          95.3%; Score 532; DB 5; Length 120;
Best Local Similarity 95.4%; Pred. No. 9.1e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYQCQYGGSPCSFGQGTKLEIK 108
   |||||
Db 61 DRFSGSGGTDFLTISRLEPEDFAVYQCQYGGSPWTFGQGTKVEIK 108
   |||||

RESULT 15
US-10-737-290-161
; Sequence 161, Application US/10737290
; Publication No. US20040253242A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Orcencia, Cecilia
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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; FILE REFERENCE: 1087-2 CIP III
; CURRENT APPLICATION NUMBER: US/10/737,290
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/452,590
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/307,724
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 130
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: recombinant Ab Vk
US-10-737-290-161
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Query Match 95.3%; Score 532; DB 5; Length 130;
Best Local Similarity 95.4%; Pred. No. 9.8e-38;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 60
   |||||
Db 23 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYATSSRATGIP 82
   |||||

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYQCQYGGSPCSFGQGTKLEIK 108
   |||||
Db 83 DRFSGSGGTDFLTISRLEPEDFAVYQCQYGGSPWTFGQGTKVEIK 130
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Search completed: April 25, 2007, 04:22:51
Job time : 39.9661 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 42 Seconds
(without alignments)
533.620 Million cell updates/sec

Title: US-10-665-383-4

Perfect score: 558

Sequence: 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLLIYATSSRATGIP 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	108	7	US-11-109-181-49
2	558	100.0	108	7	US-11-109-181-225
3	558	100.0	108	7	US-11-109-181-259
4	558	100.0	108	7	US-11-109-181-375
5	538	96.4	108	7	US-11-517-530-8
6	538	96.4	215	7	US-11-517-530-4
7	536	96.1	108	7	US-11-433-924-180
8	533	95.5	108	7	US-11-517-530-132
9	533	95.5	130	7	US-11-533-718-46
10	532	95.3	108	7	US-11-517-530-127
11	532	95.3	108	7	US-11-311-939-628
12	532	95.3	215	7	US-11-517-530-102
13	531	95.2	108	7	US-11-009-410-23
14	528	94.6	108	7	US-11-009-410-22
15	528	94.6	108	7	US-11-009-410-24
16	527	94.4	108	7	US-11-517-530-60
17	526	94.3	108	7	US-11-241-154-4
18	526	94.3	109	7	US-11-375-221-114
19	526	94.3	235	7	US-11-375-221-60
20	525	94.1	108	7	US-11-517-530-64
21	524	93.9	108	7	US-11-517-530-135
22	523	93.7	108	7	US-11-211-917-113
23	523	93.7	109	7	US-11-311-939-659
24	522.5	93.6	109	7	US-11-582-745-8
25	522	93.5	108	7	US-11-145-131A-16

ALIGNMENTS

RESULT 1

US-11-109-181-49
; Sequence 49, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-49

Query Match 100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLLIYATSSRATGIP 60

Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGAPRLLIYATSSRATGIP 60

QY 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCYQQYSSPCSGGQTKLEIK 108

Db 61 DRFSGSGSGTDFTLTISRLEPEDFAVYCYQQYSSPCSGGQTKLEIK 108

RESULT 2

US-11-109-181-225
; Sequence 225, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi

Sequence 5, Appli
Sequence 176, App
Sequence 332, App
Sequence 16, Appl
Sequence 13, Appl
Sequence 32, Appl
Sequence 6, Appl
Sequence 14, Appl
Sequence 20, Appl
Sequence 28, Appl
Sequence 68, Appl
Sequence 178, App
Sequence 48, Appl
Sequence 296, App
Sequence 16, Appl
Sequence 87, Appl
Sequence 44, Appl
Sequence 184, App

26 522 93.5 108 7 US-11-396-495-5
27 522 93.5 108 7 US-11-433-924-176
28 522 93.5 108 7 US-11-433-924-332
29 522 93.5 108 7 US-11-520-312-16
30 522 93.5 215 7 US-11-396-495-13
31 522 93.5 235 7 US-11-375-221-32
32 521.5 93.5 109 7 US-11-588-696-14
33 520.5 93.3 107 7 US-11-588-696-6
34 520 93.2 108 7 US-11-517-530-20
35 520 93.2 108 7 US-11-517-530-28
36 520 93.2 108 7 US-11-517-530-68
37 518 92.8 108 7 US-11-328-483-178
38 518 92.8 108 7 US-11-433-924-48
39 518 92.8 108 7 US-11-433-924-296
40 518 92.8 109 7 US-11-517-530-16
41 518 92.8 109 7 US-11-311-939-87
42 518 92.8 235 7 US-11-375-221-44
43 517.5 92.7 109 7 US-11-588-696-10
44 517 92.7 108 7 US-11-433-924-44
45 517 92.7 108 7 US-11-433-924-184

```

; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-225

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108

RESULT 3
US-11-109-181-259
; Sequence 259, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-259

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108

US-11-109-181-375
; Sequence 375, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-375

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108

RESULT 4
US-11-109-181-375
; Sequence 375, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-375

Query Match          100.0%; Score 558; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108

RESULT 5
US-11-517-530-8
; Sequence 8, Application US/11517530
; Publication No. US20070065444A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Amgen Fremont Inc.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
; FILE REFERENCE: ABX-PF9 PROV
; CURRENT APPLICATION NUMBER: US/11/517,530
; CURRENT FILING DATE: 2006-09-06
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Human
US-11-517-530-8

Query Match          96.4%; Score 538; DB 7; Length 108;
Best Local Similarity 96.3%; Pred. No. 3.5e-42;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108
DB 61 DRFSGSGGTDFLTISRLEPEDFAVYVYCOQYGGSPCSFGQGTGLEIK 108
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RESULT 6

US-11-517-530-4
; Sequence 4, Application US/11517530
; Publication No. US20070065444A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Amgen Fremont Inc.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
; FILE REFERENCE: ABX-PF9 PROV
; CURRENT APPLICATION NUMBER: US/11/517,530
; CURRENT FILING DATE: 2006-09-06
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Human
US-11-517-530-4

Query Match 96.4%; Score 538; DB 7; Length 215;
Best Local Similarity 96.3%; Pred. No. 7e-42; Indels 0; Gaps 0;
Matches 104; Conservative 2; Mismatches 2

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Qy 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGQTKLEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGQTKLEIK 108

RESULT 7

US-11-433-924-180
; Sequence 180, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirdid-Aimee
; APPLICANT: Foord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-180

Query Match 96.1%; Score 536; DB 7; Length 108;
Best Local Similarity 95.4%; Pred. No. 5.4e-42; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 3

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Qy 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGQTKLEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSAACSFQGQTKLEIK 108

RESULT 8

US-11-517-530-132
; Sequence 132, Application US/11517530
; Publication No. US20070065444A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Amgen Fremont Inc.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO ACTIVIN RECEPTOR-LIKE KINASE-1
; FILE REFERENCE: ABX-PF9 PROV
; CURRENT APPLICATION NUMBER: US/11/517,530
; CURRENT FILING DATE: 2006-09-06
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 132
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Human
US-11-517-530-132

Query Match 95.5%; Score 533; DB 7; Length 108;
Best Local Similarity 95.4%; Pred. No. 1e-41; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 3

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Qy 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGQTKLEIK 108
Db 61 DRFGSGSGTDFTLTISRLEPEDFAVYVCOQYGSSPCSFQGQTKLEIK 108

RESULT 9

US-11-633-716-46
; Sequence 46, Application US/11633716
; Publication No. US20070077242A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0358923
; CURRENT APPLICATION NUMBER: US/11/633,716
; CURRENT FILING DATE: 2006-12-05
; PRIOR APPLICATION NUMBER: 10/693,629
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-633-716-46

Query Match 95.5%; Score 533; DB 7; Length 130;
Best Local Similarity 95.4%; Pred. No. 1.2e-41; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 3

Qy 1 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 60
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIIYATSSRATGIP 80

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPRTFGQGTKEIK 108

Search completed: April 25, 2007, 04:27:44
Job time : 41.6441 secs

RESULT 14

US-11-009-410-22
; Sequence 22, Application US/11009410
; Publication No. US20070014724A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Alison
; APPLICANT: Williams, Denise
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: King, David
; APPLICANT: Passmore, David
; TITLE OF INVENTION: INTERFERON ALPHA ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1200696-US1
; CURRENT APPLICATION NUMBER: US/11/009,410
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/528,757
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-410-22

Query Match 94.6%; Score 528; DB 7; Length 108;
Best Local Similarity 94.4%; Pred. No. 2.9e-41;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPRTFGQGTKEIK 108

Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPRTFGQGTKEIK 108

RESULT 15

US-11-009-410-24
; Sequence 24, Application US/11009410
; Publication No. US20070014724A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Alison
; APPLICANT: Williams, Denise
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: King, David
; APPLICANT: Passmore, David
; TITLE OF INVENTION: INTERFERON ALPHA ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1200696-US1
; CURRENT APPLICATION NUMBER: US/11/009,410
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/528,757
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-410-24

Query Match 94.6%; Score 528; DB 7; Length 108;
Best Local Similarity 94.4%; Pred. No. 2.9e-41;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLIIYATSSRATGIP 60

Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLIIYATSSRATGIP 60

QY 61 DRFSGSGGTDFTLTISRLEPEDFAVYCCQYGGSPRTFGQGTKEIK 108

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 109 Seconds
(without alignments)

564.248 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKY.....VIVHYGMDVWGQGTTTIVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 200701:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*
11: Geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	100.0	126	7 ADK18597	Adk18597 Anti-huma
2	666	100.0	126	7 ADK18870	Adk18870 Anti-huma
3	666	100.0	126	7 ADK18812	Adk18812 Anti-huma
4	666	100.0	126	7 ADK18775	Adk18775 Anti-huma
5	666	100.0	126	8 ADL25412	Adl25412 Human mAb
6	605	90.8	126	7 ADK18925	Adk18925 Anti-huma
7	605	90.8	126	7 ADK18780	Adk18780 Anti-huma
8	605	90.8	126	7 ADK18616	Adk18616 Anti-huma
9	605	90.8	126	7 ADK18817	Adk18817 Anti-huma
10	605	90.8	126	8 ADL25448	Adl25448 Human mAb
11	604	90.7	126	7 ADK18864	Adk18864 Anti-huma
12	604	90.7	126	7 ADK18595	Adk18595 Anti-huma
13	604	90.7	126	7 ADK18777	Adk18777 Anti-huma
14	604	90.7	126	8 ADL25408	Adl25408 Human mAb
15	600	90.1	126	7 ADK18778	Adk18778 Anti-huma
16	600	90.1	126	7 ADK18613	Adk18613 Anti-huma
17	600	90.1	126	7 ADK18815	Adk18815 Anti-huma
18	600	90.1	126	8 ADL25464	Adl25464 Human mAb
19	593.5	89.1	125	7 ADK18614	Adk18614 Anti-huma
20	593.5	89.1	125	7 ADK18779	Adk18779 Anti-huma
21	593.5	89.1	125	7 ADK18919	Adk18919 Anti-huma
22	593.5	89.1	125	7 ADK18816	Adk18816 Anti-huma

23	593.5	89.1	125	8 ADL25444	Adl25444 Human mAb
24	593	89.0	122	6 ABR55829	AbR55829 Heavy cha
25	593	89.0	122	10 AEG17553	Aeg17553 Human ang
26	591.5	88.8	127	10 AEJ20382	Aej20382 Anti-IRTA
27	590	88.6	125	7 ADK18814	Adk18814 Anti-huma
28	584.5	87.8	119	10 AEH94456	Aeh94456 Anti-ten-
29	584.5	87.8	123	10 AEK98538	Aek98538 Human ant
30	580.5	87.2	127	7 ADK18620	Adk18620 Anti-huma
31	580.5	87.2	127	7 ADK18818	Adk18818 Anti-huma
32	580.5	87.2	127	7 ADK18781	Adk18781 Anti-huma
33	580.5	87.2	127	7 ADK18936	Adk18936 Anti-huma
34	580.5	87.2	127	8 ADL25456	Adl25456 Human mAb
35	567.5	85.2	125	7 ADK18776	Adk18776 Anti-huma
36	567.5	85.2	125	7 ADK18948	Adk18948 Anti-huma
37	567.5	85.2	125	7 ADK18624	Adk18624 Anti-huma
38	567.5	85.2	125	7 ADK18813	Adk18813 Anti-huma
39	567.5	85.2	125	8 ADL25392	Adl25392 Human mAb
40	564.5	84.8	123	10 AEK98534	Aek98534 Human ant
41	564.5	84.8	476	2 AAW88464	Aaw88464 Monoclonal
42	559.5	84.0	123	9 AED87298	Aed87298 FV2A7 hea
43	557.5	83.7	109	10 AEH94503	Aeh94503 Human Ger
44	554	83.2	450	10 AEK98141	Aek98141 Human 161
45	553.5	83.1	199	2 AAY34302	Aay34302 IgM antib

ALIGNMENTS

RESULT 1

ADK18597
ID ADK18597 standard; protein; 126 AA.
AC ADK18597;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody heavy chain protein sequence.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 21; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained from HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

```

XX SQ Sequence 126 AA;
Query Match 100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWGMWNPNSGNTGY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGGRVTMTNTSISTAYMELSLRSEDYAVYYCARDVMTITFGGVIHYGMDVWGQGT 120
DB 61 AQKFGGRVTMTNTSISTAYMELSLRSEDYAVYYCARDVMTITFGGVIHYGMDVWGQGT 120

QY 121 TTVTSS 126
DB 121 TTVTSS 126

RESULT 2
ADK18870
ID ADK18870 standard; protein; 126 AA.
XX
AC ADK18870;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #96.
XX
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US0000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 294; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 126 AA;
Query Match 100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWGMWNPNSGNTGY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGGRVTMTNTSISTAYMELSLRSEDYAVYYCARDVMTITFGGVIHYGMDVWGQGT 120
DB 61 AQKFGGRVTMTNTSISTAYMELSLRSEDYAVYYCARDVMTITFGGVIHYGMDVWGQGT 120

QY 121 TTVTSS 126
DB 121 TTVTSS 126

RESULT 3
ADK18812
ID ADK18812 standard; protein; 126 AA.
XX
AC ADK18812;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #38.
XX
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US0000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 236; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 126 AA;
Query Match 100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWGMWNPNSGNTGY 60
DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGGRVTMTNTSISTAYMELSLRSEDYAVYYCARDVMTITFGGVIHYGMDVWGQGT 120
DB 61 AQKFGGRVTMTNTSISTAYMELSLRSEDYAVYYCARDVMTITFGGVIHYGMDVWGQGT 120

QY 121 TTVTSS 126
DB 121 TTVTSS 126

```


Db 121 TTVSS 126

RESULT 4
ADK18775
ID ADK18775 standard; protein; 126 AA.

XX AC ADK18775;
XX DT 06-MAY-2004 (first entry)

XX DE Anti-human PDGF-D antibody protein related sequence #1.
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.

XX OS Homo sapiens.
XX FN WO2003057857-A2.

XX PD 17-JUL-2003.

XX PF 06-JAN-2003; 2003WO-US000398.

XX PR 07-JAN-2002; 2002US-00041860.

XX PA (ABGE-) ABGENIX INC.

XX PI Corvalan JRP, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;

XX DR WPI; 2003-587119/55.

XX PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.

XX PS Disclosure; SEQ ID NO 199; 255pp; English.

XX CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.

XX SQ Sequence 126 AA;

Query Match 100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120

QY 121 TTVSS 126
Db 121 TTVSS 126

RESULT 5
ADL25412
ID ADL25412 standard; protein; 126 AA.

AC ADL25412;

XX DT 17-JUN-2004 (first entry)

XX DE Human mAb 1.19 heavy chain variable region protein SEQ ID NO:22.

XX KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW gene therapy; human; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX PN WO2004024098-A2.

XX PD 25-MAR-2004.

XX PF 16-SEP-2003; 2003WO-US029414.

XX PR 16-SEP-2002; 2002US-0411137P.

XX PA (ABGE-) ABGENIX INC.
XX PA (CURA-) CURAGEN CORP.

XX PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;

XX DR WPI; 2004-269881/25.
XX DR N-PSDB; ADL25411.

XX PT Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.

XX PS Disclosure; SEQ ID NO 22; 115pp; English.

XX CC The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the
CC exemplification of the present invention.

XX SQ Sequence 126 AA;

Query Match 100.0%; Score 666; DB 8; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.8e-53;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60

QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVMTNTSISTAYMELSLRSEDVAVYCARDVMTFGGVIVHYGMDVWGQGT 120

QY 121 TTVSS 126
Db 121 TTVSS 126

RESULT 6
ADK18925
ID ADK18925 standard; protein; 126 AA.

PR 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
PA Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
PI WPI; 2003-587119/55.
XX
DR
XX
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 40; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 126 AA;
Query Match 90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.1e-47;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
QY 61 AQKFGQRTVMTNTSISTAYMELSSLSRSEDYAVYICARDVMITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVMTNTSISTAYMELSSLSRSEDYAVYICARDIVVVVVTATDYTYGMDVWGQGT 120
QY 121 TTVTSS 126
Db 121 TTVTSS 126
RESULT 9
ADK18817
ID ADK18817 standard; protein; 126 AA.
XX
AC ADK18817;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #43.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
XX 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
XX WPI; 2003-587119/55.
DR
XX
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 40; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 126 AA;
Query Match 90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.1e-47;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
QY 61 AQKFGQRTVMTNTSISTAYMELSSLSRSEDYAVYICARDVMITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVMTNTSISTAYMELSSLSRSEDYAVYICARDIVVVVVTATDYTYGMDVWGQGT 120
QY 121 TTVTSS 126
Db 121 TTVTSS 126
RESULT 10
ADL25448
ID ADL25448 standard; protein; 126 AA.
XX
AC ADL25448;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human mAb 1.46.1 heavy chain variable region protein SEQ ID NO:58.
XX
KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW gene therapy; human; monoclonal antibody; mAb.
XX
OS Homo sapiens.
XX
PN WO2004024098-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029414.
XX
PR 16-SEP-2002; 2002US-0411137P.
XX
PA (ABGE-) ABGENIX INC.
PA (CURA-) CURAGEN CORP.
XX
PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
XX
DR WPI; 2004-269881/25.
DR N-PSDB; ADL25447.
XX
PT Use of an antibody or its binding fragment that binds platelet derived
growth factor-DD (PDGF-DD) for preparing a medicament for treating

PT nephritis.
 PS Disclosure; SEQ ID NO 58; 115pp; English.
 XX
 CC The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of detecting nephritis; (2) a method of treating nephritis; (3) a method of inhibiting mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermatological, immunosuppressive and antiidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human monoclonal antibody (mab) variable region sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 126 AA;
 Query Match 90.8%; Score 605; DB 8; Length 126;
 Best Local Similarity 89.7%; Pred. No. 1.1e-47;
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
 QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
 DB 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
 QY 121 TTVTSS 126
 DB 121 TTVTSS 126
 RESULT 11
 ADK18864
 ID ADK18864 standard; protein; 126 AA.
 XX
 AC ADK18864;
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody protein related sequence #90.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 PN WO2003057857-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 XX
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 CC New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
 PT
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 288; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to

CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
 XX
 SQ Sequence 126 AA;
 Query Match 90.7%; Score 604; DB 7; Length 126;
 Best Local Similarity 91.3%; Pred. No. 1.4e-47;
 Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMMNPNSGNTGY 60
 QY 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
 DB 61 AQKFGQRTVMTNTSISTAYMELSLRSEDYAVYCARDVMTFGGVIVHYGMDVWGQGT 120
 QY 121 TTVTSS 126
 DB 121 TTVTSS 126
 RESULT 12
 ADK18595
 ID ADK18595 standard; protein; 126 AA.
 XX
 AC ADK18595;
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human PDGF-D antibody heavy chain protein sequence.
 XX
 KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 PN WO2003057857-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 06-JAN-2003; 2003WO-US000398.
 XX
 PR 07-JAN-2002; 2002US-00041860.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;
 XX
 DR WPI; 2003-587119/55.
 XX
 CC New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
 PT
 PT factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
 XX
 PS Disclosure; SEQ ID NO 19; 255pp; English.
 XX
 CC The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This

CC sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 90.7%; Score 604; DB 7; Length 126;
 Best Local Similarity 91.3%; Pred. No. 1.4e-47;
 Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
 DB 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
 QY 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYICARDVMITFGGVIVHYGMDVWGQGT 120
 DB 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYICARDVMITFGGVIVHYGMDVWGQGT 120
 QY 121 TTVTVSS 126
 DB 121 TTVTVSS 126

RESULT 13

ADK18777 ID ADK18777 standard; protein; 126 AA.

XX AC ADK18777;
 XX DT 06-MAY-2004 (first entry)
 XX DE Anti-human PDGF-D antibody protein related sequence #3.
 XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
 XX OS Homo sapiens.

XX WO2003057857-A2.

XX 17-JUL-2003.

XX 06-JAN-2003; 2003WO-US000398.

XX 07-JAN-2002; 2002US-00041860.

XX (ABGE-) ABGENIX INC.

XX Corvalan JRP, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
 PI Bezabeh B;

XX WPI; 2003-587119/55.

XX New human monoclonal antibody that binds to platelet-derived growth
 factor-D (PDGF-D), useful for treating chronic and recurrent human
 diseases, such as inflammation, autoimmunity and cancer.

XX Disclosure; SEQ ID NO 201; 255pp; English.

XX The invention relates to a human monoclonal antibody that binds to
 platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
 treating chronic and recurrent human diseases, such as inflammation,
 autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
 useful for modulating collagen formation, and for staging various
 cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
 generated using an active protein fragment of the gene product from the
 clone 30664188.0.99 arising in the conditioned medium obtained when
 HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
 sequence corresponds to a protein used in the invention.

XX Sequence 126 AA;

Query Match 90.7%; Score 604; DB 7; Length 126;
 Best Local Similarity 91.3%; Pred. No. 1.4e-47;
 Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
 DB 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
 QY 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYICARDVMITFGGVIVHYGMDVWGQGT 120
 DB 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYICAREGIAVAGTYYYYYGMVWGQGT 120
 QY 121 TTVTVSS 126
 DB 121 TTVTVSS 126

RESULT 14

ADL25408 ID ADL25408 standard; protein; 126 AA.

XX AC ADL25408;

XX DT 17-JUN-2004 (first entry)

XX DE Human mAb 1.18 heavy chain variable region protein SEQ ID NO:18.

XX KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
 KW nephritis; mesangial cell proliferation inhibition;
 KW mesangial proliferative glomerulonephritis; nephrotropic;
 KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
 KW gene therapy; human; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX PN WO2004024098-A2.

XX PD 25-MAR-2004.

XX 16-SEP-2003; 2003WO-US029414.

XX 16-SEP-2002; 2002US-0411137P.

XX (ABGE-) ABGENIX INC.
 XX (CURA-) CURAGEN CORP.

XX Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;

XX WPI; 2004-269881/25.

XX N-PSDB; ADL25407.

XX Use of an antibody or its binding fragment that binds platelet derived
 growth factor-DD (PDGF-DD) for preparing a medicament for treating
 nephritis.

XX Disclosure; SEQ ID NO 18; 115pp; English.

XX The present invention describes an antibody or its binding fragment that
 binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
 useful in preparing a medicament for treating nephritis. Also described:
 CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
 CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
 CC of treating mesangial proliferative glomerulonephritis. The antibody has
 CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
 CC antidiabetic activities, and can be used in gene therapy. The antibody or
 CC its binding fragment, that binds PDGF-DD, can be used in preparing a
 CC medicament for treating nephritis and related disorders, e.g., mesangial
 CC proliferative glomerulonephritis. The present sequence represents a human
 CC monoclonal antibody (mAb) variable region sequence, which is used in the
 CC exemplification of the present invention.

XX Sequence 126 AA;

Query Match 90.7%; Score 604; DB 8; Length 126;
 Best Local Similarity 91.3%; Pred. No. 1.4e-47;
 Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPCGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPCGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
QY 61 AQKFGQGRVTMTNTSISTAYMELSSLRSRSEDVAVYICARDVMITFGGVIYHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSRSEDVAVYICARDVMITFGGVIYHYGMDVWGQGT 120
QY 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 15
ADK18778
ID ADK18778 standard; protein; 126 AA.
AC ADK18778;
XX 06-MAY-2004 (first entry)
XX Anti-human PDGF-D antibody protein related sequence #4.
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
KW Homo sapiens.
OS WO2003057857-A2.
XX 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 202; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
SQ Sequence 126 AA;

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.2e-47;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 QVQLVSGAEVKKPCGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPCGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
QY 61 AQKFGQGRVTMTNTSISTAYMELSSLRSRSEDVAVYICARDVMITFGGVIYHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSRSEDVAVYICARDVMITFGGVIYHYGMDVWGQGT 120

QY 121 TTVTVSS 126
Db 121 TTVTVSS 126
Search completed: April 25, 2007, 04:05:21
Job time : 109.271 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 10 Seconds
(without alignments)
1261.509 Million cell updates/sec

Title: US-10-665-383-22
Perfect score: 666
Sequence: 1 QVQLVQSGAEVKPKPGASVKV.....VIVHYGMDVWGQGTITVTVSS 126
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569.5	85.5	127	2 S34014	Ig heavy chain V r
2	555	83.3	136	2 S31600	Ig heavy chain V r
3	530	79.6	132	2 S31596	Ig heavy chain V r
4	519.5	78.0	129	2 S46393	Ig heavy chain V r
5	517	77.6	98	2 S26918	Ig heavy chain V r
6	513	77.0	110	2 PH1670	Ig heavy chain V r
7	512	76.9	118	2 S36255	Ig heavy chain V r
8	504.5	75.8	142	2 A32483	Ig heavy chain V r
9	502	75.4	135	2 S49530	anti-Sm antibody V
10	495.5	74.4	123	2 D33548	Ig heavy chain V-1
11	493.5	74.1	129	2 S36260	Ig heavy chain V r
12	492	73.9	171	2 S23623	Ig heavy chain V r
13	486	73.0	118	2 PH1666	Ig heavy chain V r
14	486	73.0	124	2 S19665	Ig heavy chain V r
15	475.5	71.4	119	2 PH0961	Ig heavy chain V r
16	473.5	71.1	131	2 S26792	Ig heavy chain V r
17	467.5	70.2	127	2 PH0955	Ig heavy chain V r
18	466.5	70.0	122	2 S36271	Ig heavy chain V r
19	466	70.0	132	2 PH0960	Ig heavy chain V r
20	466	70.0	136	2 PH0954	Ig heavy chain V r
21	465	69.8	126	2 B33548	Ig heavy chain V-1
22	462.5	69.4	133	2 C33548	Ig heavy chain V-1
23	462.5	69.4	627	2 S14693	Ig mu chain precu
24	461	69.2	98	2 S26938	Ig heavy chain V r
25	461	69.2	114	2 PH1667	Ig heavy chain V r
26	461	69.2	117	2 S31680	Ig heavy chain V r
27	461	69.2	117	2 S18551	Ig heavy chain V r
28	461	69.2	122	2 PH0958	Ig heavy chain V r
29	460	69.1	120	2 S31999	Ig heavy chain V r

30	459.5	69.0	126	2 I44151	Ig heavy chain V r
31	457.5	68.7	160	2 PL0105	anti-PR2 erythrocy
32	456	68.5	110	2 PH1669	Ig heavy chain V r
33	453.5	68.1	109	2 PH1668	Ig heavy chain V r
34	453	68.0	98	2 S26912	Ig heavy chain V r
35	451.5	67.8	104	2 S69899	Ig heavy chain V r
36	451.5	67.8	121	2 S20783	Ig heavy chain V r
37	451.5	67.8	125	2 S68170	Ig heavy chain V r
38	451	67.7	143	1 ELHUND	Ig heavy chain pre
39	449.5	67.5	125	2 PH0957	Ig heavy chain V r
40	449.5	67.5	129	2 A33548	Ig heavy chain V-1
41	449	67.4	120	2 PH0962	Ig heavy chain V r
42	448.5	67.3	142	2 S19245	Ig heavy chain pre
43	446	67.0	120	2 S26789	Ig heavy chain V r
44	442	66.4	98	2 S26920	Ig heavy chain V r
45	442	66.4	128	2 PH0952	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S34014
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S34014; S30535
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34014
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-127 <MAR>
A:CROSS-references: UNIPARC:UPI0000176D31; EMBL:Z18321
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match		85.5%;	Score 569.5;	DB 2;	Length 127;
Best Local Similarity		85.4%;	Pred. No. 3.8e-44;		
Matches 111;		Conservative	8;	Mismatches	4;
				Indels	7;
				Gaps	2;
Qy	1	QVQLVQSGAEVKPGASVKASGYTFTSDYNVVRQATGCGLEWGMNPNSGNTGY	60		
Db	1	QVQMVQSGAEVKPGASVKASGYTFTSDYNVVRQATGCGLEWGMNPNSGNTGY	60		
Qy	61	AQKFGQRTVMTNTSISTAYMELSLRSRSDTAVYVCARDVMTFTGGVIV---	116		
Db	61	AQKFGQRTVMTNTSISTAYMELSLRSRSDTAVYFCARALSI---GVAVIRGYYYALDVM	117		
Qy	117	QGQTTTVTVSS	126		
Db	118	QGQTTTVSVSS	127		

RESULT 2

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31595
A:Accession: S31600
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:CROSS-references: UNIPARC:UPI0000116453; EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 555; DB 2; Length 136;
Best Local Similarity 85.7%; Pred. No. 8.1e-43;
Matches 108; Conservative 2; Mismatches 6; Indels 10; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 79
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICARDVMTFTGGVIVHYGMDVWGQGT 120
Db 80 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICAR-----WRDAFDWGQGT 129
Qy 121 TVTVSS 126
Db 130 MVTVSS 135

RESULT 3

S31596
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31596
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31596
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <UI>
A;Cross-references: UNIPARC:UPI0000116454; EMBL:Z14166; NID:g30996; PIDN:CAA78535.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 530; DB 2; Length 132;
Best Local Similarity 82.5%; Pred. No. 1.4e-40;
Matches 104; Conservative 3; Mismatches 5; Indels 14; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 79
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICARDVMTFTGGVIVHYGMDVWGQGT 120
Db 80 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYILAK-----APAWGQGT 125
Qy 121 TVTVSS 126
Db 126 MVTVSS 131

RESULT 4

S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: UNIPARC:UPI000011663A; EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 519.5; DB 2; Length 129;
Best Local Similarity 79.1%; Pred. No. 1.2e-39;
Matches 102; Conservative 8; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPNSSGNTY 60
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICARDVMTFT---GGVIVHYGMDVWG 117
Db 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICARDSAYYYDSSGGYSANYTMDVWG 120
Qy 118 QGTTVTVSS 126
Db 121 KGTTVTVSS 129

RESULT 5

S26918
Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TM>
A;Cross-references: UNIPARC:UPI0000031F36; EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 517; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Qy 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICAR 98
Db 61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYICAR 98

RESULT 6

PH1670
Ig heavy chain V region (clone 2A12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1670
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1670
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Cross-references: UNIPARC:UPI0000176BEB
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 513; DB 2; Length 110;
Best Local Similarity 85.6%; Pred. No. 3.8e-39;
Matches 101; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

Qy 9 AEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAQKQGRV 68
 Db 1 AEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAQKQGRV 60

Qy 69 TMTNTSISTAYMELSLRSEDYAVYCARDVMITFGGVIVHYGMDVWGQTTVTVSS 126
 Db 61 TMTNTSISTAYMELSLRSEDYAVYCAR-----GKGGEF--DIWGQTLTVSS 110

RESULT 7
 S36265
 Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C:Accession: S36265
 R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S36256; MUID:93178448; PMID:7679990
 A:Accession: S36265
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-118 <GR1>
 A:Cross-references: UNIPARC:UPI0000118DE8; EMBL:Z18846; NID:G33121; PIDN:CAA79298.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 512; DB 2; Length 118;
 Best Local Similarity 78.6%; Pred. No. 5e-39;
 Matches 99; Conservative 8; Mismatches 11; Indels 8; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCARDVMITFGGVIVHYGMDVWGQGT 120
 Db 61 AQKQGRVTITRDTSTASTAYMELSLRSEDYAVYCARDFLSGY-----LDYWGQGT 112

Qy 121 TTVTSS 126
 Db 113 LTVTSS 118

RESULT 8
 A32483
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
 C:Accession: A32483
 R:Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.
 Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
 A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
 A:Reference number: A32483; MUID:89273586; PMID:2499327
 A:Accession: A32483
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-142 <LAR>
 A:Cross-references: UNIPARC:UPI0000176C19; GB:M26463
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;25-108/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 504.5; DB 2; Length 142;
 Best Local Similarity 78.0%; Pred. No. 2.8e-38;
 Matches 99; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60
 Db 11 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 70

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCARD-VMITFGGVIVHYGMDVWGQ 119
 Db 71 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCARD-VMITFGGVIVHYGMDVWGQ 130

Qy 120 TTVTSS 126
 Db 131 LTVTSS 137

RESULT 9
 S49530
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
 C:Species: Homo sapiens (man)
 C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C:Accession: S49530
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S49530
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <MAH>
 A:Cross-references: UNIPARC:UPI00001166FF; EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 502; DB 2; Length 135;
 Best Local Similarity 77.8%; Pred. No. 4.5e-38;
 Matches 98; Conservative 6; Mismatches 12; Indels 10; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60
 Db 20 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 79

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCARDVMITFGGVIVHYGMDVWGQGT 120
 Db 80 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCAR-----ARTGNYWGQGT 129

Qy 121 TTVTSS 126
 Db 130 LTVTSS 135

RESULT 10
 D33548
 Ig heavy chain V-1 region (W1L2) - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 C:Accession: D33548
 R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
 A:Reference number: A33548; MUID:89345575; PMID:2503826
 A:Accession: D33548
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-123 <KIP>
 A:Cross-references: UNIPARC:UPI0000176909
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 495.5; DB 2; Length 123;
 Best Local Similarity 75.4%; Pred. No. 1.6e-37;
 Matches 95; Conservative 13; Mismatches 15; Indels 3; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60

Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCARDVMITFGGVIVHYGMDVWGQGT 120
 Db 11 AQKQGRVTMTNTSISTAYMELSLRSEDYAVYCAR-----LDYWGQGT 112

Db 61 AEKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCAR---ASYCGYCYFFDYWGQGT 117

QY 121 TTVTVSS 126
|||||

Db 118 LVTVSS 123

RESULT 11

S36260

Ig heavy chain V region (clone alpha-CEM4-8A) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C:Accession: S36260

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A>Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36260

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-129 <GR>

A:Cross-references: UNIPARC:UPI0000118DBB; EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 493.5; DB 2; Length 129;
Best Local Similarity 75.0%; Pred. No. 2.5e-37;
Matches 99; Conservative 9; Mismatches 15; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPKGASVKSCASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGY 60
|||||

Db 1 QVQLQSGAEVKKPKGASVKSCASGYTFTSYGISWRQAPGQGLEWMGWISAYNGNTY 60
|||||

QY 61 AQKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCARDVMTTFGGV-----IVHYGMD 114
|||||

Db 61 AQKLGQGVITRTDTSINTAYMELSLRLSDDTAVYYCARD---SFGYCSSTSCPYYYND 117
|||||

QY 115 VMGQGTTVTVSS 126
|||||

Db 118 VMGKGTTVTVSS 129
|||||

RESULT 12

S23623

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992

A>Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b

A:Reference number: S23623; MUID:92156804; PMID:1740565

A:Accession: S23623

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <OLE>

A:Cross-references: UNIPARC:UPI0000115F93; EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 492; DB 2; Length 171;
Best Local Similarity 74.6%; Pred. No. 4.5e-37;
Matches 94; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGASVKSCASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGY 60
|||||

Db 20 QVQLVQSGAEVKKPKGASVKSCASGYTFTAYQHWVRQAPGQGLEWMGWNPNSGNTGY 79
|||||

QY 61 AQKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCARDVMTTFGGVIVHYGMDVMGQGT 120
|||||

Db 80 GQKFGQGVITRTDTSINTAYMELSLRLSDDTAVYYCAIEFYDGSGLKPSDVFIDWGQGT 139
|||||

QY 121 TTVTVSS 126
|||||

Db 140 MVTVSS 145

RESULT 13

PH1666

Ig heavy chain V region (clone 6C9) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1666

R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A>Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1666

A:Molecule type: mRNA

A:Residues: 1-118 <HIL>

A:Cross-references: UNIPARC:UPI0000176BE7

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 486; DB 2; Length 118;
Best Local Similarity 79.3%; Pred. No. 1.1e-36;
Matches 96; Conservative 8; Mismatches 11; Indels 6; Gaps 2;

QY 9 AEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGV 68
|||||

Db 1 AEVKKPGASVKVSKASGYTFTSYAMHWVRQAPGQRLWGMWINAGNGNTKYAQKFGQGV 60
|||||

QY 69 TMTRTNTSISTAYMELSLRLSDDTAVYYCARDVMTTFGGVI---VHYGMDVMGQGTTVTVS 125
|||||

Db 61 TITRDTASTAYMELSLRLSDDTAVYYCAR---VTLDGKIFYYHYGMDVMGQGTTVTVS 117
|||||

QY 126 S 126

Db 118 S 118

RESULT 14

S19665

Ig heavy chain V region (alpha-phox15) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000

C:Accession: S19665; S24442

R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 591-597, 1991

A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19665

A:Molecule type: mRNA

A:Residues: 1-124 <VAR>

A:Cross-references: UNIPARC:UPI0000176B80; EMBL:X61647

R:Jones, P.T.

submitted to the EMBL Data Library, October 1991

A:Reference number: S24442

A:Accession: S24442

A:Molecule type: mRNA

A:Residues: 1-40, 'GUSGWDGSGALTMTWTQILDK', 61-118, 'T', 120-124 <JON>

A:Cross-references: UNIPARC:UPI0000115F66; EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID

A>Note: the difference for residues 41-60 results from misplacement of 10 bases in the s

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 486; DB 2; Length 124;
Best Local Similarity 75.4%; Pred. No. 1.1e-36;
Matches 95; Conservative 11; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGASVKSCASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGY 60

```
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYGISWVRQAPGQGLEWMGHSAYNGNTKY 60
QY 61 AQKFGGRVTWTRNTSISTAYMELSSLRSEDTAVYCARDVMTTFGGVIVHYGMDVWGQGT 120
Db 61 AQKLGGRVTWTRNTSISTAYMELSSLRSEDTAVYCARDVMTTFGGVIVHYGMDVWGQGT 118
QY 121 TTVVSS 126
Db 119 LTVVSS 124
```

RESULT 15

```
PH0961
IG heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0961
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <MAR>
A:Cross-references: UNIPARC:UPI0000176CES
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-107/Region: complementarity-determining 3
```

```
Query Match 71.4%; Score 475.5; DB 2; Length 119;
Best Local Similarity 76.2%; Pred. No. 9.3e-36;
Matches 96; Conservative 7; Mismatches 16; Indels 7; Gaps 1;
```

```
QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGSSVKSCASGTFSSYALSWVRQAPGQGLEWMGGIIPFGTANY 60
QY 61 AQKFGGRVTWTRNTSISTAYMELSSLRSEDTAVYCARDVMTTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGGRVTITADESTSTAYMELSSLRSEDTAVYCARDVMTTFGGVIVHYGMDVWGQGT 113
QY 121 TTVVSS 126
Db 114 TTVVSS 119
```

Search completed: April 25, 2007, 04:06:40
Job time : 9.61017 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 86 Seconds
(without alignments)
1574.822 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....VIVHGMVDVWGQGTIVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	77.6	159	2	Q96QSO_HUMAN
2	495.5	74.4	125	2	Q9UL95_HUMAN
3	488.5	73.3	244	2	Q65ZC8_HUMAN
4	480.5	72.1	119	2	Q9UL94_HUMAN
5	479	71.9	124	2	Q9UL92_HUMAN
6	459	68.9	518	2	Q6N030_HUMAN
7	453	68.0	498	2	Q6N041_HUMAN
8	452.5	67.9	497	2	Q8WY24_HUMAN
9	431.5	67.8	500	2	Q6N091_HUMAN
10	451	67.7	147	1	HVIC_HUMAN
11	441.5	66.3	119	2	Q9GYZ2_MOUSE
12	441	66.2	500	2	Q9BRV0_HUMAN
13	437	65.6	117	1	HV1B_HUMAN
14	437	65.6	117	1	HVIC_HUMAN
15	429	64.4	469	2	Q7Z7P5_HUMAN
16	425	63.8	475	2	Q6N095_HUMAN
17	420.5	63.1	458	2	Q5BZJ2_RAT
18	417.5	62.7	480	2	Q6P089_HUMAN
19	417.5	62.7	519	2	Q5EBM2_HUMAN
20	417	62.6	617	2	Q4KML5_MOUSE
21	415.5	62.4	157	2	Q95978_HUMAN
22	412	61.9	145	2	Q924Q9_MOUSE
23	408.5	61.3	117	2	Q9QXE9_MOUSE
24	408.5	61.3	458	2	Q5BK05_RAT
25	408	61.3	116	2	Q9UL89_HUMAN
26	406.5	61.0	481	2	Q91WT1_MOUSE
27	405.5	60.9	120	1	HV03_MOUSE
28	405	60.8	530	2	Q4V9V8_MOUSE
29	404.5	60.7	150	2	Q9Y298_HUMAN
30	404	60.7	145	2	Q924Q6_MOUSE
31	402.5	60.4	134	2	Q65ZR6_MOUSE

32	401.5	60.3	146	2	Q924Q3_MOUSE	Q924q3 mus musculu
33	401.5	60.3	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
34	400.5	60.1	147	2	Q925S3_MOUSE	Q925s3 mus musculu
35	400	60.1	141	2	Q924Q4_MOUSE	Q924q4 mus musculu
36	399.5	60.0	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculu
37	399	59.9	145	2	Q924R1_MOUSE	Q924r1 mus musculu
38	398.5	59.8	117	1	HV13_MOUSE	P01757 mus musculu
39	398.5	59.8	208	2	Q6ZP87_HUMAN	Q6zpb7 homo sapien
40	398	59.8	463	2	Q99LC4_MOUSE	Q99lc4 mus musculu
41	398	59.8	591	2	Q4QW0_RAT	Q4qwo0 rattus norv
42	398	59.8	613	2	O8VCX7_MOUSE	O8vcx7 mus musculu
43	397.5	59.7	117	1	HV12_MOUSE	P01756 mus musculu
44	396	59.5	120	2	Q6NSA4_HUMAN	Q6nsa4 homo sapien
45	396	59.5	145	2	Q924R4_MOUSE	Q924r4 mus musculu

ALIGNMENTS

RESULT 1
Q96QSO_HUMAN PRELIMINARY; PRT; 159 AA.
AC Q96QSO; 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 18-APR-2006, entry version 21.
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tilson M.D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; AY039025; AAK82649.1; -; mRNA.
DR HSSP; P01869; IAE6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 77.6%; Score 517; DB 2; Length 159;
Best Local Similarity 75.4%; Pred No. 2.2e-45;
Matches 98; Conservative 16; Mismatches 12; Indels 4; Gaps 1;

Qy	1	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEWMGMNPNSGNTGY	60
Db	20	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYNYMNVVRQAPGQPEWGMVINPSPGGSARY	79
Qy	61	AKQKQGRVTMTNTSISTAYNELSLRSEDATVYVCARDVMITFGVI-----VHYGMDVW	116
Db	80	SKQKQRLTMTTRDTSTVTYMDLSRLRSDTAVYFCAREMEITFGGAVSKGFFYYGMDVW	139
Qy	117	GQGTIVTVSS	126
Db	140	GQGTIVTVSS	149

RESULT 2
Q9UL95_HUMAN PRELIMINARY; PRT; 125 AA.
ID Q9UL95_HUMAN

```
AC Q9UL95;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -----
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CC -----
DE EMBL; AF035019; AAD56255.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9UL95; 1-122.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW immunoglobulin domain.
FT NON_TER 1
FT NON_TER 125
FT NON_TER 1
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 74.4%; Score 495.5; DB 2; Length 125;
Best Local Similarity 76.6%; Pred. No. 2.9e-43;
Matches 98; Conservative 9; Mismatches 16; Indels 5; Gaps 2;

Qy 1 QVQLVSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY 60
Db 1 EVQLVSGAEVKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWMNPNSGNTNY 60

Qy 61 AQKPGQGRVTMTNTSISTAYMELSLRSEDTAVYICARDVMITFGGVIVHYG--MDYWGQ 118
Db 61 AQKVGQGRVTMTTRDTTISTAYMELSLRSEDDTAVYICARS---QGGGRIAAAGDAFDIWGQ 117

Qy 119 GTTVTVSS 126
Db 118 GTMTVTSS 125

RESULT 3
Q65ZC8 HUMAN
ID Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 10.
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9732799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
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RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DE EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW immunoglobulin domain.
FT NON_TER 1
FT NON_TER 244
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 73.3%; Score 488.5; DB 2; Length 244;
Best Local Similarity 74.6%; Pred. No. 3.3e-42;
Matches 94; Conservative 14; Mismatches 13; Indels 5; Gaps 1;

Qy 1 QVQLVSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY 60
Db 1 QVQLVSGAEVKPGDSVKVSCKASGYTFSHYMHVVRQAPGQGLEWMGWDIPNNGDTRF 60

Qy 61 AQKPGQGRVTMTNTSISTAYMELSLRSEDTAVYICARDVMITFGGVIVHYGMDYWGQGT 120
Db 61 AQKPGQGRVTMTTRDTSISAAVMEVSRSLRSEDDTAVYICARE----GTGSAIYGMVWGQGT 115

Qy 121 TTVTVSS 126
Db 116 LTVTVSS 121

RESULT 4
Q9UL94 HUMAN
ID Q9UL94_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -----
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CC -----
DE EMBL; AF035020; AAD56256.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SMR; Q9UL94; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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Db 61 AQKQGRVWTRDTRSTSTVYMWELSLRSEDYVYVCARGLYVVVPAFRRF--DYWGQGT 118

Qy 121 TVTVSS 126
|||||

Db 119 LVTVSS 124

RESULT 6

Q6N030 HUMAN PRELIMINARY; PRT; 518 AA.

AC Q6N030;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 27-JUN-2006, entry version 19.

DE Hypothetical protein DKFZp686I15212.

GN Name=DKFZp686I15212;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Rectum tumor;

RG The German cDNA Consortium;

RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,

RA Mewes H.W., Weib B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major

CC histocompatibility complex class I molecules (by similarity).

CC

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CC

CC EMBL; BX640724; CAB45841.1; -; mRNA.

CC HSSP; P01861; IADQ.

CC LinkHub; Q6N030; -.

CC GO; GO:0016021; C:integral to membrane; IEA.

CC GO; GO:0016020; C:membrane; IEA.

CC GO; GO:0030106; P:MHC class I receptor activity; IEA.

CC GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.

CC GO; GO:0019885; P:antigen processing, endogenous antigen via . . ; IEA.

CC InterPro; IPR000005; HTHARAC.

CC InterPro; IPR007110; IG-like.

CC InterPro; IPR003597; IG C1-set.

CC InterPro; IPR003006; IG_MHC.

CC InterPro; IPR003599; IG_sub.

CC InterPro; IPR013106; IG_V-set.

CC Pfam; PF07654; C1-set; 3.

CC Pfam; PF07686; V-set; 1.

CC SMART; SM00409; IG; 1.

CC SMART; SM00407; IGc1; 2.

CC SMART; SM00406; IGV; 1.

CC PROSITE; PS00041; HTH ARAC FAMILY_1; UNKNOWN_1.

CC PROSITE; PS00835; IG LIKE; 4.

CC PROSITE; PS00290; IG_MHC; UNKNOWN_2.

KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;

KW Transmembrane.

QY

QY SEQUENCE 518 AA; 57020 MW; 93B5F98613BF6382 CRC64;

Query Match 68.9%; Score 459; DB 2; Length 518;

Best Local Similarity 73.0%; Pred. No. 9e-39;

Matches 92; Conservative 10; Mismatches 20; Indels 4; Gaps 135

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGNTGY 60

Db 20 QVHLVQSGAEVKKPGASVKVSCTASGYPFTNHFINWVRQAPQGSLEWMGWINTGNTKY 79

Qy 61 AQKQGRVWTRDTRSTSTVYMWELSLRSEDYVYVCARDVMITFGGVIVHYGMDVWGQGT 120

Db 80 SQKQGRVWTRDTRSTSTVYMWELSLRSEDYVYVCARDAP---QGVTTY-FDYWGQGT 135

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BX640625; CAB45779.1; -; mRNA.
DR HSP; P01751; 1A6W.
DR SMR; Q6N091; 270-478.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1-set.
DR InterPro; IPR03006; Ig MHC.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON TER 1
FT 1
SQ SEQUENCE 500 AA; 54160 MW; 3C423A17D65A41B4 CRC64;
Query Match 67.8%; Score 451.5; DB 2; Length 500;
Best Local Similarity 70.6%; Pred. No. 5.2e-38;
Matches 89; Conservative 11; Mismatches 23; Indels 3; Gaps 1;
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTVDINWVRQATGQGLEWMGNNPNSGNTGY 60
Db 38 QVQLVQSGAEVKKPGASVKVSCKASGYTFSDHSITLRLQAPGQGLEWIGMISVSGQTY 97
Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDATVYVCARDVMTFGGVIVHYGMDVWGQT 120
Db 98 AQNLQGRVTMTDTSTSTAYMELSLRSDDTAVYVCARDQSYT---TIPDAFHGQGT 154
Qy 121 TTVTVSS 126
Db 155 MTVTVSS 160
RESULT 10
HVIC_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 30-MAY-2006, entry version 47.
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).
RN [2]
RP PROTEIN SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC -----
CC HSP; P01751; INQB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR003596; Ig V-set_sub.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147
FT 19 Ig heavy chain V-I region ND.
FT /FTID=PRO_0000015246.
FT FTID=PRO_0000015246.
FT Ig-like.
FT Pyroglutamate carboxylic acid.
FT T -> V (in Ref. 2).
FT IH -> HI (in Ref. 2).
FT VG -> GV (in Ref. 2).
FT Missing (in Ref. 2).
FT NON TER 147
SQ SEQUENCE 147 AA; 16496 MW; 948F9F72A5366C20 CRC64;
Query Match 67.7%; Score 451; DB 1; Length 147;
Best Local Similarity 67.2%; Pred. No. 1.5e-38;
Matches 86; Conservative 15; Mismatches 25; Indels 2; Gaps 1;
Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTVDINWVRQATGQGLEWMGNNPNSGNTGY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFIDSYIHWRQAPGQGLEWIGMISVSGQTY 79
Qy 61 AQKQGRVTMTNTSISTAYMELSLRSEDATVYVCARDVMTFGGVIVHYGMDVWGQT 118
Db 80 APREQGRVTMTDASFSFAYMDLSRSDSDSAVFCASDPFWSDYNYFDYSYTLDVWGQ 139
Qy 119 GTTVTVSS 126
Db 140 GTTVTVSS 147
RESULT 11
Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
ID Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Peng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF282622; AAC01452.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q9GYZ2; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 66.3%; Score 441.5; DB 2; Length 119;
Best Local Similarity 67.4%; Pred. No. 1.1e-37;
Matches 87; Conservative 13; Mismatches 16; Indels 13; Gaps 2;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGMNPNSTGY 60
Db 1 QVQLVESGAERKPGASVRSCKASGYTFSTGYMNVVRQAPGHGLEWIGYINPSRGVTNY 60

Qy 61 AQKQFQRTVTRNTISITAYMELSLRSEDATVYICAR---DVMITGGVIVHYGMDVWG 117
Db 61 NQKFKQRTVTRNTKSFSTAYMELSLRSDASVYICARYDD-----HYCLDYWG 110

Qy 118 QGTTVTVSS 126
Db 111 QGTTVTVSS 119

RESULT 12
Q9BRV0 HUMAN
ID Q9BRV0 HUMAN PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 25-JUL-2006, entry version 36.
DE IGH1 protein.
GN Name=IGH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RG Mammalian Gene Collection Program Team;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RG NIH MGC Project;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC005951; AAH05951.1; -; mRNA.
DR HSSP; P01876; 1OW0.
DR SMR; Q9BRV0; 25-300, 270-478.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR013151; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig sub.
DR InterPro; IPR013106; Ig V-set.
DR InterPro; IPR003596; Ig V-set_sub.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 66.2%; Score 441; DB 2; Length 500;
Best Local Similarity 68.0%; Pred. No. 6.4e-37;
Matches 87; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGMNPNSTGY 60
Db 20 QVHLVQSGAEVMSFGASVRSCKTSGYAFHTYSIIWVRQAPQGLEWMGWSFSSDNTRF 79

Qy 61 AQKQFQRTVTRNTISITAYMELSLRSEDATVYICARV--MITFGGVIVHYGMDVWGQ 118
Db 80 AKKQFQRTVLTDTSTVYVMELSLRSDDTAVVYCARYCSYSSCONDYIIYYMDVWGK 139

Qy 119 GTTVTVSS 126
Db 140 GTTVTVSS 147

RESULT 13
HV1B HUMAN
ID HV1B HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot..
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 43.
DB Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
(VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

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CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC -----
DR EMBL: J00240; AAS2988.1; -; Genomic_DNA.
DR PIR: A02024; HVHUG.
DR HSSP: P01751; INQB.
DR LinkHub: P01743; -.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR013106; Ig V-set.
DR Pfam: PF07686; V-set; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117 Ig heavy chain V-I region HG3.
FT NON_TER 117
FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
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Query Match 65.6%; Score 437; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.2e-37;
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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DB 20 QVQLVQSGAEVKPGASVKASKASGYTFNYYHWVRQAPGQGLEWGIINPSGGSITSY 79
QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDPAVYYCAR 98
DB 80 AQKFGQRTVTRNTSISTAYMELSLRSEDPAVYYCAR 117

RESULT 14
HV1G HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1991, sequence version 1.
DT 30-MAY-2006, entry version 38.
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
[1]
RP MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus.";
RL EMBO J. 7:1047-1051(1988).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 20-116.
RX MEDLINE=93209281; PubMed=7681398;
RA Mariette X., Teapis A., Brouet J.C.;
RT "Nucleotide sequence analysis of the variable domains of four human
RT monoclonal IgM with an antibody activity to myelin-associated
RT glycoprotein.";
RL Eur. J. Immunol. 23:846-851(1993).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----

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CC EMBL: X07448; -; NOT ANNOTATED_CDS; Genomic_DNA.
DR PIR: S00476; HVH035.
DR HSSP: P01751; INQB.
DR SMR: P23083; 20-117.
DR Ensembl: ENSG00000130076; Homo sapiens.
DR LinkHub: P23083; -.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR013106; Ig V-set.
DR Pfam: PF07686; V-set; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 >117 Ig heavy chain V-I region V35.
FT NON_TER 117
FT SEQUENCE 117 AA; 13009 MW; BE61CB63F8CE97BD CRC64;
FT -----
Query Match 65.6%; Score 437; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.2e-37;
Matches 84; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVKPGASVKASKASGYTFTSYDINWVRQATGQGLEWGWMPNSGNTGY 60
DB 20 QVQLVQSGAEVKPGASVKASKASGYTFGYMHWVRQAPGQGLEWGRINPNSGTTY 79
QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDPAVYYCAR 98
DB 80 AQKFGQRTVTRNTSISTAYMELSLRSEDPAVYYCAR 117

RESULT 15
Q7Z7P5 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 27-JUN-2006, entry version 25.
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
[1]
RP TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 16 Seconds
(without alignments)
696.311 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....VIVHGMVWGQGTITVWS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	526	79.0	120	2	US-09-025-769B-36
2	526	79.0	120	2	US-09-025-769B-59
3	526	79.0	120	2	US-09-490-070A-36
4	526	79.0	120	2	US-09-490-070A-59
5	526	79.0	120	2	US-09-490-153-36
6	526	79.0	120	2	US-09-490-153-59
7	526	79.0	120	2	US-09-490-324-36
8	526	79.0	120	2	US-09-490-324-59
9	524.5	78.8	117	2	US-09-025-769B-22
10	524.5	78.8	117	2	US-09-490-070A-22
11	524.5	78.8	117	2	US-09-490-153-22
12	524.5	78.8	117	2	US-09-490-324-22
13	517	77.6	117	2	US-08-545-809A-96
14	517	77.6	117	2	US-09-515-697-96
15	509.5	76.5	470	2	US-09-859-053-28
16	508	76.3	96	2	US-10-194-975-3
17	498.5	74.8	123	2	US-10-330-613A-21
18	497.5	74.7	123	1	US-08-477-877B-94
19	497.5	74.7	123	1	US-08-472-281A-94
20	497.5	74.7	123	1	US-08-477-989B-94
21	497.5	74.7	123	2	US-09-462-140D-102
22	497.5	74.7	123	2	US-09-462-140D-105
23	491.5	73.8	125	2	US-09-199-149-3
24	491.5	73.8	129	1	US-08-561-521-45
25	491.5	73.8	129	2	US-08-525-539A-77
26	491.5	73.8	129	5	PCT-US95-01219-45

27	484.5	72.7	119	1	US-08-561-521-10	Sequence 10, Appl
28	484.5	72.7	119	5	PCT-US95-01219-10	Sequence 10, Appl
29	482	72.4	128	1	US-08-202-047-22	Sequence 22, Appl
30	482	72.4	128	2	US-08-964-690-22	Sequence 21, Appl
31	481.5	72.3	119	2	US-09-438-954-41	Sequence 42, Appl
32	478	71.8	139	1	US-08-253-877C-19	Sequence 19, Appl
33	478	71.8	139	1	US-08-452-164A-19	Sequence 19, Appl
34	478	71.8	139	2	US-08-603-024-18	Sequence 18, Appl
35	478	71.8	139	2	US-08-450-809-14	Sequence 14, Appl
36	474	71.2	118	3	US-09-875-221B-13	Sequence 13, Appl
37	470.5	70.6	119	1	US-08-300-386A-65	Sequence 65, Appl
38	470.5	70.6	119	2	US-08-931-845-65	Sequence 65, Appl
39	470.5	70.6	119	5	PCT-US95-11235-65	Sequence 65, Appl
40	470.5	70.6	121	1	US-08-202-047-23	Sequence 23, Appl
41	470.5	70.6	121	2	US-08-964-690-23	Sequence 23, Appl
42	469.5	70.5	123	1	US-08-482-882-86	Sequence 86, Appl
43	469.5	70.5	123	1	US-08-483-389-86	Sequence 86, Appl
44	469.5	70.5	123	1	US-08-487-113D-86	Sequence 86, Appl
45	469.5	70.5	123	1	US-08-473-503-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-36
; Sequence 36, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthum, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-36
Query Match 79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;

Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;
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Db |||||
1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Qy 61 AQKFGQRTVMTNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 120
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61 AQKFGQRTVMTNTSISTAYMELSSLRSEDPAVYICAR-----WGG-DGFYAMDYWGQGT 114
Qy 121 TVTVSS 126
Db |||||
115 LVTVSS 120

RESULT 2
US-09-025-769B-59
; Sequence 59, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: US/09/025,769B
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-59

Query Match 79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;
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Qy 61 AQKFGQRTVMTNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 120
Db |||||
61 AQKFGQRTVMTNTSISTAYMELSSLRSEDPAVYICAR-----WGG-DGFYAMDYWGQGT 114

Qy 121 TVTVSS 126
Db |||||
115 LVTVSS 120
RESULT 3
US-09-490-070A-36
; Sequence 36, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-490-070A-36

Query Match 79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;
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Db |||||
1 QVOLVSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGY 60
Qy 61 AQKFGQRTVMTNTSISTAYMELSSLRSEDPAVYICARDVMITFGGVIVHYGMDVWGQGT 120
Db |||||
61 AQKFGQRTVMTNTSISTAYMELSSLRSEDPAVYICAR-----WGG-DGFYAMDYWGQGT 114
Qy 121 TVTVSS 126
Db |||||
115 LVTVSS 120
RESULT 4
US-09-490-070A-59


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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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;   APPLICATION NUMBER: US/09/490,153
;   FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769B
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9090
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 120 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
;
US-09-490-153-59
Query Match          79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY      1 QVQLVQSGLAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGTNGY 60
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Db      61 AQKFGRTVTMTNTSISTAYMELSLRSRSEDTAIVYCARDVMITFGGVIVHYGMDVWGQGT 120
QY      121 TVTVSS 126
Db      115 LTVSS 120

RESULT 7
US-09-490-324-36
; Sequence 36, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,324
;   FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/025,769
;   FILING DATE: 18-FEB-1998
;   APPLICATION NUMBER: EP 95 11 3021.0
;   FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: James F. Haley, Jr., Esq.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)596-9090
;   TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 120 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
;
US-09-490-153-59
Query Match          79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY      1 QVQLVQSGLAEVKKPGASVKSCASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGTNGY 60
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Db      61 AQKFGRTVTMTNTSISTAYMELSLRSRSEDTAIVYCARDVMITFGGVIVHYGMDVWGQGT 120
QY      121 TVTVSS 126
Db      115 LTVSS 120

RESULT 8
US-09-490-324-59
; Sequence 59, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/490,324
;   FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-490-324-59

Query Match          79.0%; Score 526; DB 2; Length 120;
Best Local Similarity 83.3%; Pred. No. 5.5e-45;
Matches 105; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

Qy 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGMNPNSGNTNY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 114

Qy 121 TVTVSS 126
Db 115 LTVSS 120

RESULT 9
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11-3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

; APPLICATION NUMBER: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-22

Query Match          78.8%; Score 524.5; DB 2; Length 117;
Best Local Similarity 81.7%; Pred. No. 7.5e-45;
Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

Qy 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGMNPNSGNTNY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSLRSSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 111

Qy 121 TVTVSS 126
Db 112 LTVSS 117

RESULT 10
US-09-490-070A-22
; Sequence 22, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; WHITE & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-070A-22

Query Match      78.8%; Score 524.5; DB 2; Length 117;
Best Local Similarity 81.7%; Pred. No. 7.5e-45;
Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQAPGQGLEWGMWNPNSGNTNY 60
QY 61 AQKFGQGRVTMTRTSISTAYMELSSLSRSDTAVYICARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTRTSISTAYMELSSLSRSDTAVYICARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 112 LTVSS 117

RESULT 12
US-09-490-324-22
; Sequence 22, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-324-22

Query Match      78.8%; Score 524.5; DB 2; Length 117;
Best Local Similarity 81.7%; Pred. No. 7.5e-45;
Matches 103; Conservative 5; Mismatches 9; Indels 9; Gaps 1;

QY 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYDINWVRQAPGQGLEWGMWNPNSGNTNY 60
QY 61 AQKFGQGRVTMTRTSISTAYMELSSLSRSDTAVYICARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTRTSISTAYMELSSLSRSDTAVYICARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 112 LTVSS 117

RESULT 11
US-09-490-153-22
; Sequence 22, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-490-153-22

Query Match      78.8%; Score 524.5; DB 2; Length 117;
Best Local Similarity 81.7%; Pred. No. 7.5e-45;

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Qy	61	AKQFGQRTWMTNTSISTAYMELSSLRSDTAVYVCARDVMTFGGVVHVHYGMDVWGQGT	120
Db	61	AKQFGQRTWMTNTSISTAYMELSSLRSDTAVYVCARDVMTFGGVVHVHYGMDVWGQGT	111
Qy	121	TVTSSS	126
Db	112	LVTSSS	117

RESULT 13
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996

PCT/JPP93/00603
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29, 066
 REFERENCE/DOCKET NUMBER: 06501/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 96:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-545-809A-96

Query Match	77.6%;	Score 517;	DB 2;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 4.2e-44;		
Matches 98;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy · 1 QVQLVQSGAEVKPGASVKVSKASGYTFTSYDINWVRQATGQLEWNGMWNPSGNTGY 60
|||
Db 20 QVQLVQSGAEVKPGASVKVSKASGYTFTSYDINWVRQATGQLEWNGMWNPSGNTGY 79
|||

QY 61 AQFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCAR 98
DB 80 AQFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCAR 117

RESULT 14
US-09-515-697-96
; Sequence 96, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; Matsuda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
 SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
 NUMBER OF SEQUENCES: 145
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street -
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: Fastseq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/515,697
 FILING DATE: 29-Feb-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/545,809
 FILING DATE: 27-MAR-1996
 APPLICATION NUMBER: PCT/JP93/00603
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 06501/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 96:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 96:
 US-09-515-697-96

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Query Match      77.6%; Score 517; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.2e-44;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVSGAEVKKPKASVKVSKASGYTFTSYDINWVRQATGGLEWMCWMPNSGNTGY 60
   |||||
Db 20 QVQLVSGAEVKKPKASVKVSKASGYTFTSYDINWVRQATGGLEWMCWMPNSGNTGY 79
   |||||

Qy 61 AKQFQGRVTMTNTSISTAYMELSLRSEDATVYYCAR 98
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Db 80 AKQFQGRVTMTNTSISTAYMELSLRSEDATVYYCAR 117
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RESULT 15
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859, 053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FASTSEQ for windows Version 4.0

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; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match      76.5%; Score 509.5; DB 2; Length 470;
Best Local Similarity 78.6%; Pred. No. 1.1e-42;
Matches 99; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINNVRQATGQGLEWMGMMPNSGNTGY 60
Db 20 QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDINNVRQATGQGLEWMGMMPNSGNTGY 60
QY 61 AQKFGQRTMTTRDTSISTAYMELSLRSDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 80 AQKFGQRTMTTRDTSISTAYMELSLRSDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
QY 121 TVTVSS 126
Db 139 MTVVSS 144
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Search completed: April 25, 2007, 04:08:32
Job time : 15.839 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 47 Seconds
(without alignments)
1251.741 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....VIVHGYMDVWGQGTFTVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	666	100.0	126	4	US-10-041-860-21	Sequence 21, Appl
2	666	100.0	126	4	US-10-041-860-199	Sequence 199, App
3	666	100.0	126	4	US-10-041-860-236	Sequence 236, App
4	666	100.0	126	4	US-10-041-860-294	Sequence 294, App
5	666	100.0	126	4	US-10-041-860-22	Sequence 22, Appl
6	605	90.8	126	4	US-10-041-860-40	Sequence 40, Appl
7	605	90.8	126	4	US-10-041-860-204	Sequence 204, App
8	605	90.8	126	4	US-10-041-860-241	Sequence 241, App
9	605	90.8	126	4	US-10-041-860-349	Sequence 349, App
10	605	90.8	126	4	US-10-041-860-358	Sequence 358, App
11	604	90.7	126	4	US-10-041-860-19	Sequence 19, Appl
12	604	90.7	126	4	US-10-041-860-201	Sequence 201, App
13	604	90.7	126	4	US-10-041-860-288	Sequence 288, App
14	604	90.7	126	4	US-10-041-860-18	Sequence 18, Appl
15	600	90.1	126	4	US-10-041-860-37	Sequence 37, Appl
16	600	90.1	126	4	US-10-041-860-202	Sequence 202, App
17	600	90.1	126	4	US-10-041-860-239	Sequence 239, App
18	600	90.1	126	4	US-10-041-860-74	Sequence 74, Appl
19	593.5	89.1	125	4	US-10-041-860-38	Sequence 38, Appl
20	593.5	89.1	125	4	US-10-041-860-203	Sequence 203, App
21	593.5	89.1	125	4	US-10-041-860-240	Sequence 240, App
22	593.5	89.1	125	4	US-10-041-860-343	Sequence 343, App
23	593.5	89.1	125	4	US-10-041-860-354	Sequence 354, Appl
24	593	89.0	122	4	US-10-269-805-61	Sequence 61, Appl
25	593	89.0	122	5	US-10-982-440-61	Sequence 61, Appl
26	590	88.6	125	4	US-10-041-860-238	Sequence 238, App
27	580.5	87.2	127	4	US-10-041-860-44	Sequence 44, Appl

28	580.5	87.2	127	4	US-10-041-860-205	Sequence 205, App
29	580.5	87.2	127	4	US-10-041-860-242	Sequence 242, App
30	580.5	87.2	127	4	US-10-041-860-360	Sequence 360, App
31	580.5	87.2	127	4	US-10-041-860-66	Sequence 66, Appl
32	567.5	85.2	125	4	US-10-041-860-48	Sequence 48, Appl
33	567.5	85.2	125	4	US-10-041-860-200	Sequence 200, App
34	567.5	85.2	125	4	US-10-041-860-237	Sequence 237, App
35	567.5	85.2	125	4	US-10-041-860-372	Sequence 372, App
36	567.5	85.2	125	4	US-10-041-860-383-2	Sequence 2, Appli
37	564.5	84.8	125	3	US-09-747-669-3	Sequence 3, Appli
38	564.5	84.8	476	4	US-10-290-703-3	Sequence 3, Appli
39	549	82.4	249	3	US-09-880-748-919	Sequence 919, App
40	549	82.4	249	4	US-10-293-418-919	Sequence 919, App
41	549	82.4	249	6	US-11-054-515-919	Sequence 919, App
42	549	82.4	249	6	US-11-266-444-919	Sequence 919, App
43	545.5	81.9	242	6	US-11-090-847-93	Sequence 93, Appl
44	544	81.7	120	4	US-10-269-805-47	Sequence 47, Appl
45	544	81.7	120	5	US-10-982-440-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-10-041-860-21

; Sequence 21, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gad

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 126

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-21

Query Match 100.0%; Score 666; DB 4; Length 126;

Best Local Similarity 100.0%; Pred.No. 9.8e-56; Indels 0; Gaps 0;

Matches 126; Conservative 0; Mismatches 0;

QY 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSDINVRQATCGGLEWMGMPNSGNTGY 60

Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSDINVRQATCGGLEWMGMPNSGNTGY 60

QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCARDVMTFGVIVHYGMDVWGQGT 120

Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYVCARDVMTFGVIVHYGMDVWGQGT 120

QY 121 TVTVSS 126

Db 121 TVTVSS 126

RESULT 2

US-10-041-860-199

; Sequence 199, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

```
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-199

Query Match      100.0%; Score 666; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60

Qy 61 AOKFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 3
US-10-041-860-236
; Sequence 236, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-236

Query Match      100.0%; Score 666; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60

Qy 61 AOKFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126
```

```
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 4
US-10-041-860-294
; Sequence 294, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-294

Query Match      100.0%; Score 666; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGY 60

Qy 61 AOKFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 5
US-10-665-383-22
; Sequence 22, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-22
```

Query Match 100.0%; Score 666; DB 4; Length 126;
 Best Local Similarity 100.0%; Pred. No. 9.8e-56;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120
 Db 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
 Db 121 TTVTVSS 126

RESULT 6
 US-10-041-860-40
 ; Sequence 40, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041.860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-40

Query Match 90.8%; Score 605; DB 4; Length 126;
 Best Local Similarity 89.7%; Pred. No. 6.5e-50;
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120
 Db 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
 Db 121 TTVTVSS 126

RESULT 7
 US-10-041-860-204
 ; Sequence 204, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041.860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 204
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-204

Query Match 90.8%; Score 605; DB 4; Length 126;
 Best Local Similarity 89.7%; Pred. No. 6.5e-50;
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120
 Db 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
 Db 121 TTVTVSS 126

RESULT 8
 US-10-041-860-241
 ; Sequence 241, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041.860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 241
 ; LENGTH: 126
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-241

Query Match 90.8%; Score 605; DB 4; Length 126;
 Best Local Similarity 89.7%; Pred. No. 6.5e-50;
 Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60

Qy 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120
 Db 61 AQKQFGRVTMTNRTSISTAYMELSLRSEDYAVYCARDVMTFGGVIHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
 Db 121 TTVTVSS 126

```
RESULT 9
US-10-041-860-349
; Sequence 349, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-349

Query Match          90.8%; Score 605; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 6.5e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 11
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match          90.7%; Score 604; DB 4; Length 126;
Best Local Similarity 91.3%; Pred. No. 8.1e-50;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNGNTGY 60

Qy 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMTITFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 12
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
```


GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 49 Seconds
(without alignments)
533.620 Million cell updates/sec

Title: US-10-665-383-22

Perfect score: 666

Sequence: 1 QVQLVQSGAEVKPKGASVKV.....VIVHGMVDVWGQGTTVTVSS 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	100.0	126	7 US-11-109-181-21	Sequence 21, Appl
2	666	100.0	126	7 US-11-109-181-199	Sequence 199, App
3	666	100.0	126	7 US-11-109-181-236	Sequence 236, App
4	666	100.0	126	7 US-11-109-181-294	Sequence 294, App
5	605	90.8	126	7 US-11-109-181-40	Sequence 40, Appl
6	605	90.8	126	7 US-11-109-181-204	Sequence 204, App
7	605	90.8	126	7 US-11-109-181-241	Sequence 241, App
8	605	90.8	126	7 US-11-109-181-349	Sequence 349, App
9	604	90.7	126	7 US-11-109-181-19	Sequence 19, Appl
10	604	90.7	126	7 US-11-109-181-201	Sequence 201, App
11	604	90.7	126	7 US-11-109-181-288	Sequence 288, App
12	600	90.1	126	7 US-11-109-181-37	Sequence 37, Appl
13	600	90.1	126	7 US-11-109-181-202	Sequence 202, App
14	600	90.1	126	7 US-11-109-181-239	Sequence 239, App
15	593.5	89.1	125	7 US-11-109-181-38	Sequence 38, Appl
16	593.5	89.1	125	7 US-11-109-181-203	Sequence 203, App
17	593.5	89.1	125	7 US-11-109-181-240	Sequence 240, App
18	593.5	89.1	125	7 US-11-109-181-343	Sequence 343, App
19	591.5	88.8	126	7 US-11-433-924-94	Sequence 94, Appl
20	590	88.6	125	7 US-11-109-181-238	Sequence 238, App
21	585	87.8	122	7 US-11-433-924-254	Sequence 254, App
22	580.5	87.2	127	7 US-11-109-181-44	Sequence 44, Appl
23	580.5	87.2	127	7 US-11-109-181-205	Sequence 205, App
24	580.5	87.2	127	7 US-11-109-181-242	Sequence 242, App
25	580.5	87.2	127	7 US-11-109-181-360	Sequence 360, App

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26 567.5 85.2 125 7 US-11-109-181-48 Sequence 48, Appl
27 567.5 85.2 125 7 US-11-109-181-200 Sequence 200, App
28 567.5 85.2 125 7 US-11-109-181-237 Sequence 237, App
29 567.5 85.2 125 7 US-11-109-181-372 Sequence 372, App
30 554 83.2 450 7 US-11-396-178-20 Sequence 20, Appl
31 553.5 83.1 199 5 US-09-784-950-29 Sequence 29, Appl
32 553.5 83.1 199 7 US-11-366-003-29 Sequence 29, Appl
33 553 83.0 116 7 US-11-433-924-14 Sequence 14, Appl
34 546.5 82.1 257 7 US-11-327-917-15 Sequence 15, Appl
35 539.5 81.0 123 7 US-11-410-886-69 Sequence 69, Appl
36 539.5 81.0 449 7 US-11-410-886-22 Sequence 22, Appl
37 536.5 80.6 123 7 US-11-410-886-49 Sequence 49, Appl
38 536.5 80.6 126 7 US-11-311-939-425 Sequence 425, App
39 536.5 80.6 126 7 US-11-311-939-429 Sequence 429, App
40 536.5 80.6 449 7 US-11-410-886-6 Sequence 6, Appl
41 533.5 80.1 203 5 US-09-784-950-27 Sequence 27, Appl
42 533.5 80.1 203 7 US-11-366-003-27 Sequence 27, Appl
43 529 79.4 121 7 US-11-311-939-586 Sequence 586, App
44 526 79.0 120 7 US-11-304-986-22 Sequence 22, Appl
45 526 79.0 120 7 US-11-303-478-46 Sequence 46, Appl

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ALIGNMENTS

```

RESULT 1
US-11-109-181-21
; Sequence 21, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEROFO
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-21

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINNVROATQGLEWGMGMPNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINNVROATQGLEWGMGMPNSGNTGY 60

Qy 61 AQKFGGRVTMTNTSISTAYMELSLRSEDITAYVCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGGRVTMTNTSISTAYMELSLRSEDITAYVCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 2
US-11-109-181-199
; Sequence 199, Application US/11109181

```

```
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-199

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 4
US-11-109-181-294
; Sequence 294, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-294

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 5
US-11-109-181-40
; Sequence 40, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-236

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGY 60

Qy 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGRVTMTNTSISTAYMELSSLRSEDTAVYYCARDVMTFGGVIVHYGMDVWGQGT 120

Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 3
US-11-109-181-236
; Sequence 236, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-236

Query Match      100.0%; Score 666; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.8e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-204

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Qy 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDIVVVVVTATDYTYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 6
US-11-109-181-204
; Sequence 204, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-241

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Qy 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDIVVVVVTATDYTYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 7
US-11-109-181-241
; Sequence 241, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-241

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Qy 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDIVVVVVTATDYTYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 8
US-11-109-181-349
; Sequence 349, Application US/11/109,181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-349

Query Match          90.8%; Score 605; DB 7; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-50;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKPKGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Db 1 QVQLVQSGAEVKPKGASVKVSKASGYFTSYDINWVRQATGQGLEWMGWNPNNSGNTGY 60
Qy 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQGVMTTRNTSISTAYMELSLRSEDATVYYCARDIVVVVVTATDYTYGMDVWGQGT 120
Qy 121 TTVTVSS 126
Db 121 TTVTVSS 126
```

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; ORGANISM: homo sapiens
US-11-109-181-349

Query Match
Best Local Similarity 90.8%; Score 605; DB 7; Length 126;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60

QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDIVVVVTTATDYDYYGMDVWGQGT 120

QY 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 9
US-11-109-181-19
; Sequence 19, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-19

Query Match
Best Local Similarity 90.7%; Score 604; DB 7; Length 126;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60

QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICAREGIAVAGTYYYYYGMVWGQGT 120

QY 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 10
US-11-109-181-201
; Sequence 201, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
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; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-201

Query Match
Best Local Similarity 90.7%; Score 604; DB 7; Length 126;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60

QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICAREGIAVAGTYYYYYGMVWGQGT 120

QY 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 11
US-11-109-181-288
; Sequence 288, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-288

Query Match
Best Local Similarity 90.7%; Score 604; DB 7; Length 126;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60

QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICAREGIAVAGTYYYYYGMVWGQGT 120

QY 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 12
US-11-109-181-288
; Sequence 288, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-288

Query Match
Best Local Similarity 90.7%; Score 604; DB 7; Length 126;
Matches 115; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60
Db 1 QVQLVSGAEVKKPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMMNPNSGNTGY 60

QY 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICARDVMTITFGGVIVHYGMDVWGQGT 120
Db 61 AQKFGQRTVTRNTSISTAYMELSLRSEDATVYICAREGIAVAGTYYYYYGMVWGQGT 120

QY 121 TTVTVSS 126
Db 121 TTVTVSS 126

RESULT 13
US-11-109-181-201
; Sequence 201, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
```

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QY 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

```

```

RESULT 12
US-11-109-181-37
; Sequence 37, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-37

```

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Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
QY 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

```

```

RESULT 13
US-11-109-181-202
; Sequence 202, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860

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; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-202

```

```

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
QY 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

```

```

RESULT 14
US-11-109-181-239
; Sequence 239, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 239
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-239

```

```

Query Match 90.1%; Score 600; DB 7; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.8e-50;
Matches 112; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWNPNPNSGNTGY 60
QY 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
Db 61 AOKFQGRVTMTNTSISTAYMELSLRSEDATVYYCARDVMTFGGVIHVHGMVWGQGT 120
QY 121 TVTVSS 126
Db 121 TVTVSS 126

RESULT 15
US-11-109-181-38

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; Sequence 38, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-38

Query Match      89.1%; Score 593.5; DB 7; Length 125;
Best Local Similarity 91.3%; Pred. No. 1.6e-49;
Matches 115; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Qy      1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWMPNPSGNTGY 60
Db      1 QVQLVQSGAEVKPKGASVKVCKASGYTFTSYDINWVRQATGQGLEWGWMPNPSGNTGY 60

Qy      61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVMCGQT 120
Db      61 AQKFGQGVTVTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFGGVIVHYGMDVMCGQT 119

Qy      121 TTVTVSS 126
Db      120 TTVTVSS 125

```

Search completed: April 25, 2007, 04:27:44
Job time : 49.5847 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 93 Seconds
(without alignments)
564.248 Million cell updates/sec

Title: US-10-665-383-24
Perfect score: 558
Sequence: 1 DIQWTSFSLASVGRVT.....CLOHNSDPCSFQGTKEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_200701.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*
11: Geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	107	7	ADK18598
2	558	100.0	107	7	ADK18838
3	558	100.0	107	7	ADK18837
4	558	100.0	107	7	ADK18873
5	558	100.0	107	7	ADK18803
6	558	100.0	107	8	ADL25414
7	542	97.1	107	8	ADS84414
8	542	97.1	107	8	ADR68556
9	542	97.1	234	8	ADS84470
10	542	97.1	234	8	ADR68612
11	539	96.6	107	8	ADS84402
12	539	96.6	107	8	ADR68544
13	539	96.6	234	8	ADR68452
14	539	96.6	234	8	ADR68594
15	528	94.6	107	7	ADK18841
16	528	94.6	108	10	Aej60732
17	528	94.6	236	5	ABG77160
18	528	94.6	236	8	ADR28582
19	528	94.6	236	10	Aef54367
20	528	94.6	236	10	Aef54346
21	528	94.6	236	10	Aef34918
22	528	94.6	236	10	AEL09667

23	528	94.6	236	10	AEL59900
24	527	94.4	107	5	ABG30494
25	527	94.4	108	8	ADS16571
26	525	94.1	107	7	ADC99789
27	525	94.1	107	7	ADD05393
28	525	94.1	107	7	ADF09831
29	525	94.1	107	7	ADK18842
30	525	94.1	107	7	ADK18916
31	525	94.1	107	7	ADK18892
32	525	94.1	107	7	ADK18612
33	525	94.1	107	7	ADK18602
34	525	94.1	107	7	ADK18810
35	525	94.1	107	7	ADK18844
36	525	94.1	107	7	ADK18808
37	525	94.1	107	7	ADK18807
38	525	94.1	107	7	ADK18604
39	525	94.1	107	7	ADP03996
40	525	94.1	107	8	ADL25422
41	525	94.1	107	8	ADL25426
42	525	94.1	107	8	ADL25442
43	525	94.1	107	8	ADO07289
44	525	94.1	107	8	ADP22368
45	525	94.1	107	8	ADP22401

ALIGNMENTS

RESULT 1
ADK18598
ID ADK18598 standard; protein; 107 AA.
XX
AC ADK18598;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody light chain protein sequence.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 22; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.

DR N-PSDB; ADL25413.
XX Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.
XX
XX Disclosure; SEQ ID NO 24; 115pp; English.
XX
XX The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 107 AA;
SQ
Query Match 100.0%; Score 558; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 2e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFSGSGGTDTFTLTISLQPEDFATYVYCLQHNSDPCSFQGTGLEIR 107
Db 61 RFSGSGGTDTFTLTISLQPEDFATYVYCLQHNSDPCSFQGTGLEIR 107
RESULT 7
ADS84414
ID ADS84414 standard; protein; 107 AA.
XX
XX ADS84414;
XX
XX 18-NOV-2004 (first entry)
XX Human anti-EPO-R antibody light chain variable region SEQ ID NO:53.
XX human; erythropoietin receptor; EPO receptor;
XX erythropoietin receptor binding antibody; EPO receptor binding antibody;
XX antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
XX wound healing; neural cell damage protection;
XX neural tissue damage protection; brain injury; spinal cord injury;
XX stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
XX
XX Homo sapiens.
XX
XX WO2004035603-A2.
XX
XX 29-APR-2004.
XX
XX 14-OCT-2003; 2003WO-US032243.
XX
XX 14-OCT-2002; 2002US-00269711.
XX
XX 10-OCT-2003; 2003US-00684109.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
XX WPI; 2004-348433/32.
XX N-PSDB; ADS84413.
XX
XX New antibodies that bind to or activate an endogenous human

erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g. anemia.
Claim 10; SEQ ID NO 53; 192pp; English.
The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (EPO) receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The EPO receptor binding antibody has antianaemic, neuroprotective and vulnary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dysfunctional EPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-EPO-R antibody light chain variable region, which is given in the exemplification of the present invention.
Sequence 107 AA;
Query Match 97.1%; Score 542; DB 8; Length 107;
Best Local Similarity 97.2%; Pred. No. 3.1e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Qy 61 RFSGSGGTDTFTLTISLQPEDFATYVYCLQHNSDPCSFQGTGLEIR 107
Db 61 RFSGSGGTDTFTLTISLQPEDFATYVYCLQHNSDPCSFQGTGLEIR 107
RESULT 8
ADR68556
ID ADR68556 standard; protein; 107 AA.
XX
XX ADR68556;
XX
XX 02-DEC-2004 (first entry)
XX
XX Anti-EPO-R-antibody light chain variable region seqid 53.
XX antianaemic; respiratory; vulnary; gene therapy; vaccine;
XX erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
XX hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
XX wound healing; neural cell damage; tissue damage; brain injury;
XX spinal cord injury; stroke; anti-EPO-R-antibody; light chain;
XX variable region.
XX
XX Homo sapiens.
XX
XX US2004175379-A1.
XX
XX 09-SEP-2004.
XX
XX 10-OCT-2003; 2003US-00684109.
XX

PR 14-OCT-2002; 2002US-0418031P.
 XX (DEVIR/) DEVRIES P J.
 PA (OSTR/) OSTROW D H.
 PA (REIL/) REILLY E B.
 PA (GREG/) GREEN L L.
 PA (WIEL/) WIELER J.
 XX
 XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 PI WPI: 2004-661369/64.
 DR N-PSDB; ADR68555.
 XX
 XX New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 XX
 XX Claim 10; SEQ ID NO 53; 156pp; English.
 XX
 XX The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R
 CC -antibody light chain variable region.
 XX
 XX Sequence 107 AA;
 CC
 CC Query Match 97.1%; Score 542; DB 8; Length 107;
 CC Best Local Similarity 97.2%; Pred. No. 3.1e-33;
 CC Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWYQKPKAPKRLIYAASLSQSGVPS 60
 CC
 CC 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWYQKPKAPKRLIYAASLSQSGVPS 60
 CC
 CC 61 RFSGSGSGTFTLTISLQPEDPATYTCLOHNSDPCSFQGGTKLEIR 107
 CC
 CC 61 RFSGSGSGTFTLTISLQPEDPATYTCLOHNSYPCSFQGGTKLEIK 107
 CC
 CC RESULT 9
 CC ADS84470
 CC ID ADS84470 standard; protein; 234 AA.
 CC
 CC AC ADS84470;
 CC
 CC 18-NOV-2004 (first entry)
 CC
 CC Human anti-EPO-R antibody Ab467 light chain SEQ ID NO:109.

human; erythropoietin receptor; EPO receptor; erythropoietin binding antibody; antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia; wound healing; neural cell damage protection; brain injury; spinal cord injury; stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 Homo sapiens.
 WO2004035603-A2.
 29-APR-2004.
 14-OCT-2003; 2003WO-US032243.
 14-OCT-2002; 2002US-00269711.
 10-OCT-2003; 2003US-00684109.
 (ABBO) ABBOTT LAB.
 Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 WPI: 2004-348433/32.
 N-PSDB; ADS84468, ADS84469.
 New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor; e.g. anemia.
 Disclosure; SEQ ID NO 109; 192pp; English.
 The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (EPO) receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The EPO receptor binding antibody has antianaemic, neuroprotective and vulnerary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dysfunctional EPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-EPO-R antibody light chain, which is given in the exemplification of the present invention.
 Sequence 234 AA;
 Query Match 97.1%; Score 542; DB 8; Length 234;
 Best Local Similarity 97.2%; Pred. No. 6.4e-33;
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWYQKPKAPKRLIYAASLSQSGVPS 60
 21 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLWYQKPKAPKRLIYAASLSQSGVPS 80
 61 RFSGSGSGTFTLTISLQPEDPATYTCLOHNSDPCSFQGGTKLEIR 107
 81 RFSGSGSGTFTLTISLQPEDPATYTCLOHNSYPCSFQGGTKLEIK 127

RESULT 10
ADR68612
ID ADR68612 standard; protein; 234 AA.
XX
AC ADR68612;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human antibody Ab467 light chain polypeptide seqid 109.
XX
XX
KW antianemic; respiratory; vulnery; gene therapy; vaccine;
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
KW wound healing; neural cell damage; tissue damage; brain injury;
KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
KW Ab467.
XX
XX
OS Homo sapiens.
XX
PN US2004175379-A1.
XX
PD 09-SEP-2004.
XX
PF 10-OCT-2003; 2003US-00684109.
XX
PR 14-OCT-2002; 2002US-0418031P.
XX
PA (DEVRIE) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
XX
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX
XX
DR WPI; 2004-661369/64.
DR N-PSDB; ADR68610.
XX
XX
PT New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal, useful for treating a mammal suffering aplasia or anemia.
XX
PS Disclosure; SEQ ID NO 109; 156pp; English.
XX
XX
CC The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This sequence represents a human Ab467 antibody
CC light chain polypeptide.
XX

SO Sequence 234 AA;
Query Match 97.1%; Score 542; DB 8; Length 234;
Best Local Similarity 97.2%; Pred. No. 6.4e-33;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSSLSASVGRVVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
Db 21 DIQWTQSPSSLSASVGRVVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 80
Qy 61 RFSGSGSGTFTLTISSLPEDFAFYCLOHNSDPCSPGQGTGLR 107
Db 81 RFSGSGSGTFTLTISSLPEDFAFYCLOHNSYPCSPGQGTGLR 127
RESULT 11
ADS84402
ID ADS84402 standard; protein; 107 AA.
XX
AC ADS84402;
XX
XX 18-NOV-2004 (first entry)
DT
DE Human anti-EPO-R antibody light chain variable region SEQ ID NO:41.
XX
KW human; erythropoietin receptor; EPO receptor;
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
KW antianemic; neuroprotective; vulnery; gene therapy; aplasia; anaemia;
KW wound healing; neural cell damage protection;
KW neural tissue damage protection; brain injury; spinal cord injury;
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
XX
OS Homo sapiens.
XX
PN WO2004035603-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032243.
XX
PR 14-OCT-2002; 2002US-00269711.
PR 10-OCT-2003; 2003US-00684109.
XX
XX (ABBO) ABBOTT LAB.
XX
PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
XX
XX
DR WPI; 2004-348433/32.
DR N-PSDB; ADS84401.
XX
PT New antibodies that bind to or activate an endogenous human
PT erythropoietin receptor, useful for diagnosing, preventing or treating
PT disorders associated with dysfunctional erythropoietin receptor, e.g.
XX
XX
PS Claim 10; SEQ ID NO 41; 192pp; English.
XX
XX The present invention describes an antibody or its fragment that binds to
XX or activates an endogenous activity of a human erythropoietin (EPO)
XX receptor in a mammal, but does not interact with a peptide having a
XX sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
XX methods of modulating or activating an endogenous activity of a human EPO
XX receptor in a mammal, comprising administering to the mammal a
XX therapeutic amount of the above antibody or its fragment to modulate or
XX activate the receptor; (2) a method of treating a mammal suffering from
XX aplasia, comprising administering to the mammal a therapeutic amount of
XX the above antibody or its fragment to modulate or activate the receptor;
XX (3) a pharmaceutical composition comprising a therapeutic amount of the
XX above antibody or antibody fragment, and a pharmaceutical excipient; (4)
XX an isolated and purified polynucleotide sequence; and (5) an isolated and
XX complements and degenerate codon equivalents; and (5) an isolated and
XX purified amino acid sequence, and their fragments. The EPO receptor
XX binding antibody has antianemic, neuroprotective and vulnery

CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain variable region, which is given in the exemplification of the
 CC present invention.

XX Sequence 107 AA;

Query Match 96.6%; Score 539; DB 8; Length 107;
 Best Local Similarity 96.3%; Pred. No. 5.2e-33;
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
 QY 61 RFGSGSGTDTLTISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107
 DB 61 RFGSGSGTDTLTISLQPEDFATYYCLOHNSDPCSFQGGTKLEIK 107

RESULT 12

AD868544
 ID AD868544 standard; protein; 107 AA.
 XX
 AC AD868544;
 DT 02-DEC-2004 (first entry)
 XX Anti-EPO-R-antibody light chain variable region seqid 41.
 DE
 XX antianaemic; respiratory; vulnary; gene therapy; vaccine;
 XX erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 KW wound healing; neural cell damage; tissue damage; brain injury;
 KW spinal cord injury; stroke; anti-EPO-R-antibody; light chain;
 KW variable region.
 XX
 OS Homo sapiens.
 XX
 XX US2004175379-A1.
 XX
 XX 09-SEP-2004.
 XX
 XX 10-OCT-2003; 2003US-00684109.
 XX
 XX 14-OCT-2002; 2002US-0418031P.
 XX
 XX (DEVIR/) DEVIRIES P J.
 XX (OSTR/) OSTROW D H.
 XX (REIL/) REILLY E B.
 XX (GREE/) GREEN L L.
 XX (WIEL/) WIELER J.

Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 WPI; 2004-661369/64.
 DR N-PSDB; ADR68543.
 DR
 XX New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 XX
 PS Claim 10; SEQ ID NO 41; 156pp; English.
 XX
 XX The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain

CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This is the amino acid sequence of an anti-EPO-R
 CC -antibody light chain variable region.

XX Sequence 107 AA;

Query Match 96.6%; Score 539; DB 8; Length 107;
 Best Local Similarity 96.3%; Pred. No. 5.2e-33;
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQGVPS 60
 QY 61 RFGSGSGTDTLTISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107
 DB 61 RFGSGSGTDTLTISLQPEDFATYYCLOHNSDPCSFQGGTKLEIK 107

RESULT 13

AD84452
 ID AD84452 standard; protein; 234 AA.
 XX
 AC AD84452;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 XX Human anti-EPO-R antibody Ab390 light chain SEQ ID NO:91.
 XX
 XX human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 XX
 OS Homo sapiens.
 XX
 XX WO2004035603-A2.
 XX
 XX 29-APR-2004.
 XX
 XX 14-OCT-2003; 2003WO-US032243.
 XX
 XX 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX

DR WPI; 2004-348433/32.
 DR N-PSDB; ADS84450, ADS84451.
 XX
 PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anaemia.
 XX
 PS Disclosure; SEQ ID NO 91; 192pp; English.
 XX
 CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianaemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 234 AA;
 Query Match 96.6%; Score 539; DB 8; Length 234;
 Best Local Similarity 96.3%; Pred. No. 1.1e-32;
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
 DB 21 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 80
 QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTQKLEIR 107
 DB 81 RFSGSGSGTDFTLTISLQPEDFATYYCLOHNSYPCSFQGTQKLEIK 127
 RESULT 14
 ADR68594
 ID ADR68594 standard; protein; 234 AA.
 XX
 AC ADR68594;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human antibody Ab390 light chain polypeptide seqid 91.
 XX
 KW antianaemic; respiratory; vulnerary; gene therapy; vaccine;
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 KW wound healing; neural cell damage; tissue damage; brain injury;
 KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
 KW AB390; ds.
 XX
 OS Homo sapiens.
 XX
 PN US2004175379-A1.
 XX
 PD 09-SEP-2004.

XX
 PF 10-OCT-2003; 2003US-00684109.
 XX
 PR 14-OCT-2002; 2002US-0418031P.
 XX
 PA (DEVRA/) DEVRIES P J.
 PA (OSTR/) OSTROW D H.
 PA (REIL/) REILLY E B.
 PA (GREE/) GREEN L L.
 PA (WIEL/) WIELER J.
 XX
 XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 PI WPI; 2004-661369/64.
 XX N-PSDB; ADR68592.
 DR
 DR New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 PT
 XX Disclosure; SEQ ID NO 91; 156pp; English.
 PS
 XX The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a pharmaceutical amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence represents a human Ab390 antibody
 CC heavy chain polynucleotide.
 XX
 SQ Sequence 234 AA;
 Query Match 96.6%; Score 539; DB 8; Length 234;
 Best Local Similarity 96.3%; Pred. No. 1.1e-32;
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60
 DB 21 DIQWTQSPSSLSASVGDRTVITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 80
 QY 61 RFSGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTQKLEIR 107
 DB 81 RFSGSGSGTDFTLTISLQPEDFATYYCLOHNSYPCSFQGTQKLEIK 127
 RESULT 15
 ADR68594
 ID ADR68594 standard; protein; 107 AA.
 XX
 AC ADR68594;
 XX
 DT 06-MAY-2004 (first entry)

XX Anti-human PDGF-D antibody protein related sequence #67.
DE antiinflammatory; immunomodulator; cytostatic; gene therapy.
KW Homo sapiens.
XX WO2003057857-A2.
XX 17-JUL-2003.
XX 06-JAN-2003; 2003WO-US000398.
XX 07-JAN-2002; 2002US-00041860.
XX (ABGE-) ABGENIX INC.
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX Disclosure; SEQ ID NO 265; 255pp; English.
XX The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX Sequence 107 AA;
SQ
Query Match 94.6%; Score 528; DB 7; Length 107;
Best Local Similarity 95.3%; Pred. No. 3.5e-32;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQWTQSPSLASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60
Db 1 DIQWTQSPSLASVGDRTVITCRASQGIKNDLQWYQKPKAPKRLIYAASLSQGVPS 60
Qy 61 RFSGSGGTDTLTITSSLPQEDFATYYCLOHNSDPCSPFGGQTKLEIR 107
Db 61 RFSGSGGTDTLTITSSLPQEDFATYYCLOHNSYPWTFGGQTKLEIK 107

Search completed: April 25, 2007, 04:05:19
Job time : 93.7938 secs

GenCore version 6.2.1

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 8 Seconds
(without alignments)
1261.509 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQHNSDPCSFQGTGKLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	89.8	125	2 S40353	Ig kappa chain V-J
2	494	88.5	108	1 KIHUGL	Ig kappa chain V-I
3	489	87.6	108	1 KIHUEU	Ig kappa chain V-I
4	488	87.5	123	2 S40313	Ig kappa chain V-J
5	484	86.7	107	2 S36269	Ig kappa chain V
6	481	86.2	117	2 S41809	Ig kappa chain V r
7	480	86.0	107	2 S36282	Ig kappa chain V
8	471	84.4	129	2 S40369	Ig kappa chain - h
9	468	83.9	123	2 S40331	Ig kappa chain - h
10	467	83.7	127	2 S40367	Ig kappa chain V-J
11	466	83.5	126	2 S40335	Ig kappa chain V-J
12	463	83.0	108	2 S36279	Ig kappa chain V
13	463	83.0	108	2 B49047	Ig kappa chain V r
14	461	82.6	131	2 S40352	Ig kappa chain V-J
15	460	82.4	114	2 S46377	Ig kappa chain V-J
16	459	82.3	125	2 S40333	Ig kappa chain V-J
17	456	81.7	108	2 S19674	Ig kappa chain V r
18	455.5	81.6	107	2 S36275	Ig kappa chain V
19	455	81.5	108	1 KIHUHU	Ig kappa chain V-I
20	455	81.5	125	2 S40349	Ig kappa chain V-J
21	454	81.4	95	2 S69898	Ig kappa chain V-J
22	453	81.2	132	2 S40334	Ig kappa chain - h
23	452	81.0	117	2 S42264	Ig kappa chain V r
24	451	80.8	117	2 S46376	Ig kappa chain V-J
25	450.5	80.7	107	2 S47183	Ig kappa chain - h
26	449	80.5	107	2 I69017	anti-HIV1 envelope
27	449	80.5	129	1 KIHUWK	Ig kappa chain pre
28	447.5	80.2	124	2 S40336	Ig kappa chain V-J
29	447	80.1	107	2 S36284	Ig kappa chain V

30	447	80.1	108	1 KIHUEU	Ig kappa chain V-I
31	447	80.1	108	2 S47182	Ig kappa chain - h
32	447	80.1	129	2 S52793	Ig kappa chain V r
33	446	79.9	108	1 KIHUBN	Ig kappa chain V-I
34	446	79.9	129	2 S40317	Ig kappa chain - h
35	445	79.7	105	2 S36266	Ig lambda chain V
36	445	79.7	117	2 S46371	Ig kappa chain V-J
37	444	79.6	108	2 S44122	Ig kappa chain V r
38	444	79.6	122	2 S40314	Ig kappa chain - h
39	443.5	79.5	108	2 S30521	Ig kappa chain V r
40	443	79.4	120	2 S46370	Ig kappa chain V-J
41	442	79.2	117	2 C21056	Ig kappa chain pre
42	441	79.0	124	2 S40318	Ig kappa chain V r
43	441	79.0	128	2 S46372	Ig light chain var
44	438	78.5	129	2 S52789	Ig kappa chain V r
45	437	78.3	109	2 S31998	Ig kappa chain - h

ALIGNMENTS

RESULT 1

S40353

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40353

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40353

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: UNIPARC:UPI0000176CAE; EMBL:X72463

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

P:30-104/Domain: immunoglobulin homology <IMM>

Query Match

89.8%; Score 501; DB 2; Length 125;

Best Local Similarity 89.7%; Pred. No. 3.2e-36;

Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 60

DB 15 DIQMTQSPSSLSASVGRVTITCRASQIGRNDLQWYQKPGKAPKRLIYAASSLSQSGVPS 74

QY 61 RFSGSGSGTDFTLTISSLQPEDPATYCYCLQHNSDPCSFQGTGKLEIR 107

DB 75 RFSGSGSGTEFTLTISGLQPEDPATYCYCLQHNSDPCSFQGTGKLEIR 121

RESULT 2

KIHUGL

Ig kappa chain V-I region (Gal) - human (tentative sequence)

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C:Accession: A01867

R:Laure, C.J.; Watanabe, S.; Hilgemann, N.

Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973

A:Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I.

A:Reference number: A01867; MUID:75059122; PMID:4215718

A:Accession: A01867

A:Molecule type: protein

A:Residues: 1-108 <LAU>

A:Cross-references: UNIPROT:P01599; UNIPARC:UPI000012E142

A>Note: the C region of this chain has the Inv (3) marker

C:Comment: This chain was isolated from a Waldenstrom's macroglobulin.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status predicted

Query Match 88.5%; Score 494; DB 1; Length 108;
 Best Local Similarity 89.7%; Pred. No. 1.1e-35;
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFLTITISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107

Db 61 RFGSGGAGTEFTLTITISLQPEDFATYYCLOHNSDPCSFQGGTKVEIK 107

RESULT 3

KLHWE

Ig kappa chain V-I region (WEA) - human

C:Species: Homo sapiens (man)

C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

C:Accession: A01876

R:Goni, F.; Frangione, B.

Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983

A:Title: Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with

A:Reference number: A93964; MUID:83273707; PMID:6410398

A:Accession: A01876

A:Molecule type: protein

A:Residues: 1-108 <CON>

A:Cross-references: UNIPROT:P01610; UNIPARC:UPI000012E14C

C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated galactose

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status predicted

Query Match 87.6%; Score 489; DB 1; Length 108;
 Best Local Similarity 86.9%; Pred. No. 3e-35;
 Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGTAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDFLTITISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107

Db 61 RFGSGSGTEFTLTITISLQPEDFATYYCLOHNSDPCSFQGGTKVEIK 107

RESULT 4

S40313

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40313

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40313

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: UNIPARC:UPI000011613P; EMBL:X72423; NID:9441314; PIDN:CAAS1091.1; PII
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 488; DB 2; Length 123;
 Best Local Similarity 87.9%; Pred. No. 4.1e-35;
 Matches 94; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 17 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 76

Qy 61 RFGSGSGTDFLTITISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107

Db 77 RFGSGSGTEFTLTITISLQPEDFATYYCLOHNSDPCSFQGGTKVEIK 123

RESULT 5

S36269

Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C:Accession: S36269

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36269

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-107 <GRI>

A:Cross-references: UNIPARC:UPI0000118DF1; EMBL:Z18838; NID:933422; PIDN:CAA79290.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

86.7%; Score 484; DB 2; Length 107;

Best Local Similarity 88.8%; Pred. No. 8e-35;

Matches 95; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIKNDLWYQKPGKAPKRLIYTSSLSQGVPS 60

Qy 61 RFGSGSGTDFLTITISLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107

Db 61 RFGSGSGTDFLTITISLQPEDFATYYCLOHNSDPCSFQGGTKLEIK 107

RESULT 6

S41809

Ig kappa chain V region A30 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S41809

R:Huber, C.; Schaeuble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Zacht

Eur. J. Immunol. 23, 2868-2875, 1993

A:Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequence

A:Reference number: S41809; MUID:94039386; PMID:8223863

A:Accession: S41809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <HUB>

A:Cross-references: UNIPARC:UPI000011618B; EMBL:X72808; NID:9415383; PIDN:CAAS1328.1; PII

C:Genetics:

A:Introns: 19/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match

86.2%; Score 481; DB 2; Length 117;

Best Local Similarity 97.9%; Pred. No. 1.6e-34;

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Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 60
Db 23 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 82
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSDP 95
Db 83 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSTP 117

RESULT 7
S36262
Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36262
R:Griffiths, A.D.; Malnqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36262
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: UNIPARC:UPI0000176D2C; EMBL:Z18842
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 480; DB 2; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.2e-34;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIVMTQSPSSLSASIGDRVTITCRSGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 60
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSDPSCFSGQGTKEIR 107
Db 61 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSTPPTFGGQTKVEIK 107

RESULT 8
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 471; DB 2; Length 129;
Best Local Similarity 86.9%; Pred. No. 1.2e-33;
Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 60
Db 22 DIQMTQSPSSLSASVGRVTITCRASHVISNHLVFWQKPGKAPKSLIYAASLSQGVPS 81
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSDPSCFSGQGTKEIR 107
Db 82 RFSGSGSGTDFLTITSSLOPEDFATYICQYNSIPYTFGGQTKLEIK 128
```

```
RESULT 9
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 468; DB 2; Length 123;
Best Local Similarity 86.9%; Pred. No. 2.1e-33;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 60
Db 17 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKRLIYAASLSQGVPS 76
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSDPSCFSGQGTKEIR 107
Db 77 RFSGSGSGTDFLTITSSLOPEDFATYICQSYSTPRTFGGQTKVEIK 123

RESULT 10
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 467; DB 2; Length 127;
Best Local Similarity 86.0%; Pred. No. 2.7e-33;
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGYQKPGKAPKRLIYAASLSQGVPS 60
Db 18 DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKRLIYAASLSQGVPS 77
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYICLQHNSDPSCFSGQGTKEIR 107
Db 78 RFSGSGSGTDFLTITSSLOPEDFATYICQSYNTPTWTFGGQTKVEIK 124

RESULT 11
S40335
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40335
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
```


Db 8 IQMRQSPSSLSASVGRVTTTCRASQIRNDLGNQKPKAPKLLIYAASSLESQVPSR 67

Qy 62 FSGSGTDFTLTISSLOPEDPATYVCLOHNSDPCSFQGTKEI 106

Db 68 FSGSGTDFTLTISSLOPEDPATYVCLOHNSDPCSFQGTKEI 112

Search completed: April 25, 2007, 04:06:39
Job time : 9.16102 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 73 Seconds
(without alignments)
1574.822 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQNSDPCSFQGTKLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	91.6	236	2	Q502W4 HUMAN
2	494	88.5	108	1	KV1G HUMAN
3	480	87.8	236	2	Q6GMW1 HUMAN
4	489	87.6	108	1	KV1R HUMAN
5	469	84.1	108	2	Q9UL70 HUMAN
6	462	82.8	236	2	Q6GMX8 HUMAN
7	456	81.7	236	2	Q7Z3Y4 HUMAN
8	455	81.5	108	1	KV1H HUMAN
9	453	81.2	108	2	Q9UL77 HUMAN
10	453	81.2	236	2	Q6FIH7 HUMAN
11	449	80.5	129	1	KV1W HUMAN
12	447	80.1	108	1	KV1F HUMAN
13	446	79.9	108	1	KV1V HUMAN
14	445	79.8	107	2	Q6SA9 HUMAN
15	445	79.7	244	2	Q6SZC8 HUMAN
16	440	78.9	236	2	Q6GMX9 HUMAN
17	440	78.9	236	2	Q6GMX0 HUMAN
18	437	78.3	240	2	Q6SZC9 HUMAN
19	434	77.9	107	2	Q9UL81 HUMAN
20	431	77.2	108	1	KV1O HUMAN
21	430	77.1	234	2	QSEFE6 HUMAN
22	429	76.9	108	2	Q9UL79 HUMAN
23	429	76.9	236	2	Q6PIT5 HUMAN
24	427	76.5	108	1	KV1N HUMAN
25	427	76.5	117	1	KV1I HUMAN
26	426	76.3	108	1	KV1C HUMAN
27	426	76.3	108	1	KV1E HUMAN
28	426	76.3	236	2	Q6PIH4 HUMAN
29	425	76.2	108	1	KV1M HUMAN
30	425	76.2	108	1	KV1Q HUMAN
31	424	76.0	108	1	KV1S HUMAN

32	423	75.8	108	1	KV1B HUMAN	P01594 homo sapien
33	423	75.8	108	1	KV1D HUMAN	P80362 homo sapien
34	419.5	75.2	107	1	KV1D HUMAN	P01596 homo sapien
35	418	74.9	108	1	KV1L HUMAN	P01604 homo sapien
36	418	74.9	234	2	Q7Z473 HUMAN	Q72473 homo sapien
37	416	74.6	108	1	KV1A HUMAN	P01593 homo sapien
38	416	74.6	108	1	KV1K HUMAN	P01603 homo sapien
39	415	74.4	108	1	KV1P HUMAN	P01608 homo sapien
40	410	73.5	117	1	KV1J HUMAN	P01602 homo sapien
41	410	73.5	129	1	KV1X HUMAN	P04432 homo sapien
42	405	72.6	189	2	Q569T7 HUMAN	Q56917 homo sapien
43	397	71.1	108	1	KV5S MOUSE	P01652 mus musculus
44	396	71.0	116	2	Q96FF6 HUMAN	Q96pf6 homo sapien
45	395.5	70.9	109	1	KV1T HUMAN	P01612 homo sapien

ALIGNMENTS

RESULT 1

Q502W4 HUMAN
AC Q502W4; PRELIMINARY; PRT; 236 AA.
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2005, sequence version 1.
DT 11-JUL-2006, entry version 13.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
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EMBL: BC095489; AAH95489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.

DR GO: 0030106; F:MHC class I receptor activity; IEA.
 DR GO: 0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO: 0019883; P:antigen processing, endogenous antigen via . . .; IEA.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig C1-set.
 DR InterPro: IPR003006; Ig MHC.
 DR InterPro: IPR003599; Ig sub.
 DR InterPro: IPR013106; Ig V-set.
 DR InterPro: IPR003596; Ig V-set_sub.
 DR Pfam: PF07654; C1-set; 1.
 DR Pfam: PF07686; V-set; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00407; IGc1; 1.
 DR SMART: SM00406; IGv; 1.
 DR PROSITE: PS0835; IG LIKE; 2.
 DR PROSITE: PS0290; IG_MHC; UNKNOWN 1.
 KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
 SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 91.6%; Score 511; DB 2; Length 236;
 Best Local Similarity 91.6%; Pred No. 2, 1e-44;
 Matches 98; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60
 Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 82

QY 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTKEIR 107
 Db 83 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTKEIR 129

RESULT 2
 KVIG HUMAN STANDARD; PRT; 108 AA.
 AC P01599;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 25-JUL-2006, entry version 43.
 DE Ig kappa chain V-I region Gal.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=75059122; PubMed=4215718;
 RA Laure C.J., Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
 kappa-type, subgroup I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -!- MISCELLANEOUS: This chain was isolated from a Waldenström's
 macroglobulin.
 CC
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 CC
 CC PIR: A01867; K1HUGL.
 DR HSSP; P01607; 1BWW.
 DR SMR; P01599; 1-108.
 DR GO: 0005576; C:extracellular region; NAS.
 DR GO: 0003823; F:antigen binding; NAS.
 DR GO: 0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003599; Ig sub.
 DR InterPro: IPR013106; Ig V-set.
 DR Pfam: PF07686; V-set; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00406; IGv; 1.

DR PROSITE; PS0835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 FT CHAIN 1 >108
 FT Ig kappa chain V-I region Gal.
 FT /FTID=PRO_0000059743.
 FT Framework-1.
 FT REGION 1 23
 FT REGION 24 34
 FT REGION 35 49
 FT REGION 50 56
 FT REGION 57 88
 FT REGION 89 97
 FT REGION 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 88.5%; Score 494; DB 1; Length 108;
 Best Local Similarity 89.7%; Pred. No. 4, 9e-43;
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTKEIR 107
 Db 61 RFGSGSGTDTLTITSLQPEDFATYICLQHNSDPCSFQGTKEIR 107

RESULT 3
 Q6GMW1 HUMAN PRELIMINARY; PRT; 236 AA.
 ID Q6GMW1_HUMAN
 AC Q6GMW1
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 27-JUN-2006, sequence version 1.
 DE IGKC protein.
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major

```

CC      histocompatibility complex class I molecules (By similarity).
CC      -----
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CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: BC073791; AAH73791.1; -; mRNA.
DR      SMR: Q6GHW1; 24-236.
DR      Ensemble: ENSG00000163245; Homo sapiens.
DR      GO: GO:0016021; C:integral to membrane; IEA.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0030106; F:MHC class I receptor activity; IEA.
DR      GO: GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR      GO: GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003597; IG C1-set.
DR      InterPro: IPR003006; IG_MHC.
DR      InterPro: IPR003599; IG_sub.
DR      InterPro: IPR013106; IG_V-set.
DR      InterPro: IPR003596; IG_V-set_sub.
DR      Pfam: PF07654; C1-set; 1.
DR      Pfam: PF07686; V-set; 1.
DR      SMART: SM00409; IG; 1.
DR      SMART: SM00407; IGc1; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS00835; IG LIKE; 2.
DR      PROSITE: PS00290; IG_MHC; UNKNOWN 1.
KW      Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ      SEQUENCE 236 AA; 25751 MW; 5BP56A087AFAC437 CRC64;

Query Match      87.8%; Score 490; DB 2; Length 236;
Best Local Similarity 90.6%; Pred. No. 3.1e-42;
Matches 96; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 IQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPSR 61
DB      24 IQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPSR 83
QY      62 FSGSGSGTDTLTITSSLPQEDFATYYCLOHNSDPCSFQGTGKLEIR 107
DB      84 FSGSGSGTDTLTITSSLPQEDFATYYCLOHNSDPCSFQGTGKLEIR 129

RESULT 4
KVLR_HUMAN
ID      KVLR_HUMAN STANDARD; PRT; 108 AA.
AC      P01610;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      30-MAY-2006, entry version 39.
DE      Ig kappa chain V-I region WEA.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RX      MEDLINE=83273707; PubMed=6410398;
RA      Goni F., Frangione B.;
RT      "Amino acid sequence of the Fv region of a human monoclonal IgM
RT      (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT      in Klebsiella polysaccharides K30 and K33.";
RL      Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC      -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC      against 3,4-pyruvylated galactose and isolated from a patient with
CC      Waldenstrom's macroglobulinemia.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      PIR: A01876; KIHUWE.
DR      HSSP: P80362; LWTL.
DR      SMR: P01610; 1-108.

```

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DR      GO: GO:0005576; C:extracellular region; NAS.
DR      GO: GO:0003823; F:antigen binding; NAS.
DR      GO: GO:0006955; P:immune response; NAS.
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003599; IG_sub.
DR      InterPro: IPR013106; IG_V-set.
DR      InterPro: IPR003596; IG_V-set_sub.
DR      Pfam: PF07686; V-set; 1.
DR      SMART: SM00409; IG; 1.
DR      SMART: SM00406; IGV; 1.
DR      PROSITE: PS00835; IG LIKE; 1.
KW      Direct protein sequencing; Immunoglobulin domain;
KW      Immunoglobulin V region; Monoclonal antibody.
FT      CHAIN 1 >108
FT      REGION 1 23
FT      REGION 24 34
FT      REGION 35 49
FT      REGION 50 56
FT      REGION 57 88
FT      REGION 89 97
FT      REGION 98 107
FT      DISULFID 23 88
FT      NON_TER 108 108
SQ      SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match      87.6%; Score 489; DB 1; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.6e-42;
Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY      1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
DB      1 DIQWTQSPSSLSASVGRVITTCRASQGIKNDLQWYQKPGKAPKRLIYGATSLQGVPS 60
QY      61 RFSGSGSGTDTLTITSSLPQEDFATYYCLOHNSDPCSFQGTGKLEIR 107
DB      61 RFSGSGSGTDTLTITSSLPQEDFATYYCLOHNSDPCSFQGTGKLEIR 107

RESULT 5
Q9UL70_HUMAN
ID      Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC      Q9UL70;
DT      01-MAY-2000, integrated into UniProtKB/TREMBL.
DT      01-MAY-2000, sequence version 1.
DT      18-APR-2006, entry version 23.
DE      Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA      Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,
RA      Diamond B.;
RT      "Molecular characteristics of antibodies bearing an anti-DNA-
RT      associated idiotype.";
RL      J. Exp. Med. 174:1639-1652(1991).
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: AF035044; AAD56280.1; -; mRNA.

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DR PIR, PH0863;
DR HGSP; P01607; 1BW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 84.1%; Score 469; DB 2; Length 108;
Best Local Similarity 86.0%; Pred. No. 1.9e-40;
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQIGIRNDLGYOQKPKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQIGISNYLAWYQOKPKGKSLIYAASLTLSQSGVPS 60

QY 61 RFSGSGGTDFTLTISSLPQEDFATYYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGGTDFTLTISSLPQEDVATYYCQKNSAPRTFGPTKLEIK 107

RESULT 6
ID Q6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 19-JUN-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 27-JUN-2006, entry version 22.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deng J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
```

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CC histocompatibility complex class I molecules (By similarity).
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC073764; AAH73764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0030106; F: MHC class I receptor activity; IEA.
DR GO; GO:0019885; P: antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019883; P: antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1-set.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559BFC9 CRC64;

Query Match 82.8%; Score 462; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 2.5e-39;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQIGIRNDLGYOQKPKAPKRLIYAASSLSQSGVPS 60
Db 23 DIQMTQSPSSLSASVGRVITTCRASQIGISNYLAWYQOKPKGKSLIYAASLTLSQSGVPS 82

QY 61 RFSGSGGTDFTLTISSLPQEDFATYYCLOHNSDPCSFQGGTKLEIR 107
Db 83 RFSGSGGTDFTLTISSLPQEDFATYYCQAHSPFTFGPTKVDIK 129

RESULT 7
Q723Y4 HUMAN
ID Q723Y4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 27-JUN-2006, entry version 25.
DE Hypothetical protein.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deng J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
```

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skeletal Muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC
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 CC
 CC EMBL; BC005332; AAH05332.1; -; mRNA.
 DR HSSP; P01834; 1HEZ.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig C1-set.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
 KW Transmembrane.
 SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;
 Query Match 81.7%; Score 456; DB 2; Length 236;
 Best Local Similarity 84.1%; Pred.No.1e-38;
 Matches 90; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
 Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLAWFQKPKAPKSLIYGASSLSQSGVQS 82
 QY 61 RFSGSGSGTDFTLTISLSQPEDPATYICLOHNSDPCSFQGGTKLEIR 107
 Db 83 RFSGSGSGTDFTLTISLSQPEDPATYICQYKSPVPTFGQGTKEIK 129
 RESULT 8
 KVIH_HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
 DT 21-JUL-1986, sequence version 1.
 DT 25-JUL-2006, entry version 47.
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=71032830; PubMed=4057974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-

RT chain of subgroup I (Bence-Jones protein Hau): subdivision within
 RT subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC
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 CC
 CC PIR; A01868; KIHUHU.
 DR PDB; 1F6L; X-ray; L=1-89.
 DR SMR; P01600; 1-108.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin domain; Immunoglobulin V region.
 FT CHAIN 1 >108
 FT /FTID=PRO_0000059744.
 FT Framework-1.
 FT REGION 1 23
 FT REGION 24 34
 FT REGION 35 49
 FT REGION 50 56
 FT REGION 57 88
 FT REGION 89 97
 FT REGION 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 FT STRAND 4 7
 FT STRAND 9 12
 FT TURN 15 16
 FT TURN 19 27
 FT TURN 30 31
 FT STRAND 33 38
 FT STRAND 38 38
 FT TURN 40 41
 FT STRAND 45 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT STRAND 77 77
 FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 92 95
 FT STRAND 98 98
 FT STRAND 102 105
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
 Query Match 81.5%; Score 455; DB 1; Length 108;
 Best Local Similarity 84.1%; Pred.No.5.3e-39;
 Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQGIKNDLQWYQKPKAPKRLIYAASSLSQSGVPS 60
 Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSISSYLSWYQKPKAPQVLIYAASSLSQSGVPS 60
 QY 61 RFSGSGSGTDFTLTISLSQPEDPATYICLOHNSDPCSFQGGTKLEIR 107
 Db 61 RFSGSGSGTDFTLTISLSQPEDPATYICQYKSPVPTFGQGTKEIK 107
 RESULT 9


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DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR RZPD-ProtExp; T2901; -.
DR RZPD-ProtExp; T2902; -.
DR RZPD-ProtExp; W0370; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG sub.
DR InterPro; IPR013106; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS0290; IG MHC; UNKNOWN 1.
KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 81.2%; Score 453; DB 2; Length 236;
Best Local Similarity 83.2%; Pred. No. 2.1e-38;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLGMWYQKPKAPKELIYAASLSQSGVPS 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 DIQLTQSPFSLASVGDRTVITCRASQGISSYLAWYQKPKAPNLLIYAASLTQSGVPS 82
QY 61 RFSGSGSGTDFTLTISSLQPEDPATYICLQHNSDPCSFQGTQKLEIR 107
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 RFSGSGSGTDFTLTISSLQPEDPATYICLQHNSSPPTFGGTYKVEIK 129

RESULT 11
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 27-JUN-2006, entry version 43.
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
DR PIR; A01883; KIHUK.
DR HSSP; P01607; IBHW.
DR SMR; P04431; 23-129.
DR Ensemble; ENSG00000163245; Homo sapiens.
DR LinkHub; P04431; -.
DR RZPD-ProtExp; IOH14191; -.
DR RZPD-ProtExp; IOH21663; -.
DR RZPD-ProtExp; IOH23035; -.
DR RZPD-ProtExp; IOH23055; -.
DR RZPD-ProtExp; IOH23077; -.
DR RZPD-ProtExp; IOH23168; -.
DR RZPD-ProtExp; IOH23177; -.
DR RZPD-ProtExp; IOH23178; -.
DR RZPD-ProtExp; IOH23179; -.
DR RZPD-ProtExp; IOH29440; -.
DR RZPD-ProtExp; IOH40810; -.
DR RZPD-ProtExp; IOH7177; -.
DR RZPD-ProtExp; T2893; -.

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DR RZPD-ProtExp; T2896; -.
DR RZPD-ProtExp; T2901; -.
DR RZPD-ProtExp; T2902; -.
DR RZPD-ProtExp; W0370; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG sub.
DR InterPro; IPR013106; IG_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT REGION 23 45 Ig kappa chain V-I region Walker.
FT REGION 46 56 /FTID=PRO_0000015170.
FT REGION 57 71 Framework-1.
FT REGION 72 78 Complementarity-determining-1.
FT REGION 79 110 Complementarity-determining-2.
FT REGION 111 119 Complementarity-determining-3.
FT REGION 120 129 Complementarity-determining-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941PA07D4AFC2F9 CRC64;

Query Match 80.5%; Score 449; DB 1; Length 129;
Best Local Similarity 85.0%; Pred. No. 2.7e-38;
Matches 91; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

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Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 DIQMTQSPSSLSASVGDRTVITCRASQGISNYLWYQKPKAPKLLIYAASLSQSGVTS 82
QY 61 RFSGSGSGTDFTLTISSLQPEDPATYICLQHNSDPCSFQGTQKLEIR 107
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 RFSGSGSGTDFTLTISSLQPEDSATYICQSYSTLTITFGQGTRELK 129

RESULT 12
KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01538;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 40.
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----

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DR PIR: A90562; K1HUEU.
DR HSP: P01607; 1BW.

DR SMR: P01598; 1-107.
DR Ensembl: ENSG00000163245; Homo sapiens.

DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.

DR GO: GO:0006955; P:immune response; NAS.
DR GO: GO:0007110; Ig-like.

DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003599; Ig sub.

DR InterPro: IPR013106; Ig V-set.
DR InterPro: IPR003596; Ig V-set_sub.

DR Pfam: PF07686; V-set; 1.
DR SMART: SM00409; IG; 1.

DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.

DR Direct.protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.

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FT /FTID=PRO:0000059742.

FT REGION 1 23
FT REGION 24 34
FT REGION 35 49

FT REGION 50 56
FT REGION 57 88
FT REGION 89 97

FT REGION 98 107
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FT DISULFID 23 88

FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

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Best Local Similarity 80.4%; Pred. No. 3.6e-38;

Matches 86; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
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DB 1 DIQMTQSPSTLSASVGRVTITCRASQSIINTLAWYQKPKAPKRLIMYKASSLSQSGVPS 60

QY 61 RFGSGSGTDTLTITSLQPEDFATYICLQNSDPCSPFGQGTKEIR 107

DB 61 RFGSGSGTETLTITSLQPDDEFATYICQYNSDKMFGQGTKEVK 107

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AC P04430;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.

DT 13-AUG-1987, sequence version 1.
DT 30-MAY-2006, entry version 41.

DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP PROTEIN SEQUENCE.

RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dulet F.E., O'Connor T.P., Benson M.D.;

RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).

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DR PIR: A01878; K1HUBN.
DR HSP: P80362; 1WTL.

DR SMR: P04430; 1-108.
DR GO: GO:0005576; C:extracellular region; NAS.

DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003599; Ig sub.

DR InterPro: IPR013106; Ig V-set.
DR InterPro: IPR003596; Ig V-set_sub.

DR Pfam: PF07686; V-set; 1.
DR SMART: SM00409; IG; 1.

DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.

DR Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.

FT CHAIN 1 >108
FT Ig kappa chain V-I region BAN.
FT /FTID=PRO:0000059756.

FT REGION 1 23
FT REGION 24 34
FT REGION 35 49

FT REGION 50 56
FT REGION 57 88
FT REGION 89 97

FT REGION 98 107
FT REGION 98 107
FT DISULFID 23 88

FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.9%; Score 446; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 4.6e-38;

Matches 85; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
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DB 1 DIQMTQSPSSLSASVGRVTITCRASQSVYVYVAVFQKPKAPKSLIYDASTLQSGVPS 60

QY 61 RFGSGSGTDTLTITSLQPEDFATYICLQNSDPCSPFGQGTKEIR 107

DB 61 NFTGSGSGTDTLTITSLQPEDFATYICQYNSPYTFQGTKEVQIK 107

RESULT 14
Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.

AC Q96SA9;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.
DT 18-APR-2006, entry version 19.

DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
DE Variable region (Fragment).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98375893; PubMed=9712075;

RA Aderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;

RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin

RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).

RN [2]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=92387224; PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;

RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene

RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).

RN [3]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;

RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are

RT	distributed over a large portion of the V kappa locus and do not show
RT	somatic mutation."
RL	Eur. J. Immunol. 23:391-397(1993).
RR	[4]
RR	NUCLEOTIDE SEQUENCE.
RP	MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RX	Manheimer-Lory A., Katz J.B., Pillingner M., Ghossein C., Smith A.,
RA	Diamond B.;
RA	"Molecular characteristics of antibodies bearing an anti-DNA-
RT	associated idiotype.";
RT	J. Exp. Med. 174:1639-1652(1991).
RL	[5]
RR	NUCLEOTIDE SEQUENCE.
RP	MEDLINE=91243737; PubMed=1903706;
RX	Blaision G., Kuntz J.L., Pasquali J.L.;
RA	"Molecular analysis of V kappa III variable regions of polyclonal
RT	rheumatoid factors during rheumatoid arthritis.";
RT	Eur. J. Immunol. 21:1221-1227(1991).
RR	CC
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CC	-----
DR	EWBL; U96396; AAB68785.1; -; mRNA.
DR	PIR; B49047; B49047.
DR	PIR; PH0867; PH0867.
DR	PIR; S16840; S16840.
DR	PIR; S31977; S31977.
DR	PIR; S34083; S34083.
DR	PIR; S34086; S34086.
DR	HSSP; P01607; 1BWV.
DR	SMR; Q96SA9; 1-107.
DR	Ensembl; ENSG00000163245; Homo sapiens.
DR	LinkHub; Q96SA9; -.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003599; Ig_sub.
DR	InterPro; IPR013106; Ig_V-set.
DR	InterPro; IPR003596; Ig_V-set_sub.
DR	pFam; PF07686; V-set; 1.
DR	SMART; SM00409; IG; 1.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	immunoglobulin domain.
FT	NON_TER 1
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SQ	SEQUENCE 107 AA; 115520 MW; 4BB43E9C5B577F16 CRC64;

[illegible]

RESULT	15	
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ID	Q65ZC8_HUMAN	PRELIMINARY; PRT; 244 AA.
AC	Q65ZC8;	
DT	11-OCT-2004,	integrated into UniProtKB/TrEMBL.
DT	11-OCT-2004,	sequence version 1.
DT	18-APR-2005,	entry version 10.
DE	Single-chain Fv (Fragment).	
DE	Name=scFv;	
GN	GN	
OS	Hom sapiens (Human).	
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria;	Euarchontoglires; Primates; Haplorrhini;
OC	Catarrhini; Homidae;	Homo.
OX	NCBI TaxID=9606;	

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[1]
RN      NUCLEOTIDE SEQUENCE.
RP      MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RX      Kontermann R.E., Wing M.G., Winter G.;
RA      "Complement recruitment using bispecific diabodies.";
RL      Nat. Biotechnol. 15:629-631(1997).
CC      -----
CC      Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL: Y13057; CAA73500.1; -; mRNA.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003599; Ig_sub.
DR      InterPro; IPR013106; Ig V-set.
DR      InterPro; IPR003596; Ig V-set_sub.
DR      Pfam: PF07686; V-set; 2.
DR      SMART; SM00409; IG; 2.
DR      SMART; SMO0406; IGV; 2.
DR      PROSITE; PS00835; IG_LIKE; 2.
DR      Immunoglobulin domain.
FT      NON_TER      1
FT      TER          244
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Best Local Similarity 80.4%; Pred. No. 1.5e-37;
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps

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QY      61 RFSGSGSGTDFTLTITSLQPEDPATYCYCLOHNSDPGCSFGOGTKLEIR 107
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      197 RFSGSGSGTDFTLTITSLQDDPATYCYQSYNPITFGGGTKLEIK 243
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Job time : 73.8446 secs

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Search completed: April 25, 2007, 04:06:33
Job time : 73.8446 secs

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 13 Seconds
(without alignments)
696.311 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC Celerra_SIDS3/prodata/2/iaa/5 COMB.pep.*
- 2: /EMC Celerra_SIDS3/prodata/2/iaa/6 COMB.pep.*
- 3: /EMC Celerra_SIDS3/prodata/2/iaa/7 COMB.pep.*
- 4: /EMC Celerra_SIDS3/prodata/2/iaa/H COMB.pep.*
- 5: /EMC Celerra_SIDS3/prodata/2/iaa/PTUS COMB.pep.*
- 6: /EMC Celerra_SIDS3/prodata/2/iaa/RE COMB.pep.*
- 7: /EMC Celerra_SIDS3/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	94.1	107	2	US-10-330-613A-18
2	519	93.0	107	2	US-10-330-613A-14
3	490	87.8	107	2	US-09-240-274-29
4	490	87.8	107	2	US-09-848-798-29
5	481	86.2	95	2	US-10-194-975-59
6	481	86.2	95	2	US-10-330-613A-47
7	481	86.2	95	2	US-10-330-613A-48
8	481	86.2	95	2	US-10-330-613A-51
9	481	86.2	95	2	US-10-330-613A-52
10	481	86.2	107	2	US-08-599-226-9
11	481	86.2	107	2	US-09-125-098-9
12	481	86.2	107	2	US-09-540-018-9
13	480	86.0	109	2	US-09-025-769B-28
14	480	86.0	109	2	US-09-025-769B-43
15	480	86.0	109	2	US-08-490-070A-28
16	480	86.0	109	2	US-09-490-070A-43
17	480	86.0	109	2	US-09-490-153-28
18	480	86.0	109	2	US-09-490-153-43
19	480	86.0	109	2	US-09-490-324-28
20	480	86.0	109	2	US-09-490-324-43
21	479	85.8	107	1	US-07-934-373C-18
22	479	85.8	107	2	US-08-437-642B-18
23	479	85.8	107	2	US-08-146-206C-18
24	479	85.8	107	2	US-09-648-067A-14
25	479	85.8	107	2	US-09-705-686-18
26	479	85.8	107	2	US-09-705-392A-18

27	479	85.8	107	2	US-09-705-398-18	Sequence 18, Appl
28	479	85.8	107	2	US-09-602-812A-5	Sequence 5, Appl
29	479	85.8	107	5	PCT-US93-07832-18	Sequence 18, Appl
30	479	85.8	108	2	US-08-974-899-3	Sequence 3, Appl
31	479	85.8	108	2	US-09-795-798-3	Sequence 3, Appl
32	479	85.8	108	2	US-08-908-469-12	Sequence 12, Appl
33	477	85.5	107	2	US-08-599-226-1	Sequence 1, Appl
34	477	85.5	107	2	US-09-125-098-1	Sequence 1, Appl
35	477	85.5	107	2	US-09-540-018-1	Sequence 10, Appl
36	476	85.3	109	2	US-10-330-613A-10	Sequence 13, Appl
37	475	85.1	107	2	US-09-644-668A-13	Sequence 32, Appl
38	474	84.9	108	1	US-08-378-939-32	Sequence 34, Appl
39	474	84.9	108	1	US-08-378-939-34	Sequence 8, Appl
40	473	84.8	108	2	US-09-920-262A-8	Sequence 24, Appl
41	472	84.6	108	1	US-08-378-939-24	Sequence 3, Appl
42	472	84.6	109	1	US-07-934-373C-3	Sequence 3, Appl
43	472	84.6	109	2	US-08-437-642B-3	Sequence 3, Appl
44	472	84.6	109	2	US-08-146-206C-3	Sequence 3, Appl
45	472	84.6	109	2	US-09-705-686-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-10-330-613A-18
; Sequence 18, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-18

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Best Local Similarity 94.4%; Pred. No. 8.4e-42;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Db 1 DIQWTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

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Db 61 RFSGSGSGTFTLTISLQPEDFATYTCLOHNSYPTWTFGQGTQKVEIK 107

RESULT 2

US-10-330-613A-14
; Sequence 14, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 107

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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-14

Query Match      93.0%; Score 519; DB 2; Length 107;
Best Local Similarity 93.5%; Pred. No. 3e-41;
Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGTKVEIK 107

RESULT 3
US-09-240-274-29
; Sequence 29, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-29

Query Match      87.8%; Score 490; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPSRF 62
Db 2 ELTQSPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPSRF 61

Qy 63 SGSGSGTDFTLTISLQPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 62 SGSGSGTEFTLTISLQPEDSATYCYCLOHNSFPWTFQGGTKVEIK 106

RESULT 4
US-09-848-798-29
; Sequence 29, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

Query Match      87.8%; Score 490; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPSRF 62
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Qy 63 SGSGSGTDFTLTISLQPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 62 SGSGSGTEFTLTISLQPEDSATYCYCLOHNSFPWTFQGGTKVEIK 106

RESULT 5
US-10-194-975-59
; Sequence 59, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-59

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYCYCLOHNSDP 95
Db 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYP 95

RESULT 6
US-10-330-613A-47
; Sequence 47, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-47
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; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-848-798-29

Query Match      87.8%; Score 490; DB 2; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 QMTQSPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPSRF 62
Db 2 ELTQSPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPSRF 61

Qy 63 SGSGSGTDFTLTISLQPEDFATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 62 SGSGSGTEFTLTISLQPEDSATYCYCLOHNSFPWTFQGGTKVEIK 106

RESULT 5
US-10-194-975-59
; Sequence 59, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-59

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQWTPSSLSASVGDRTVITTCRASQGIKNDLGMWYQKPGKAPKRLIYAASSLSQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYCYCLOHNSDP 95
Db 61 RFGSGSGTEFTLTISLQPEDFATYCYCLOHNSYP 95

RESULT 6
US-10-330-613A-47
; Sequence 47, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-47
```



```
Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSDP 95
Db 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSYP 95

RESULT 7
US-10-330-613A-48
; Sequence 48, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-48

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSDP 95
Db 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSYP 95

RESULT 8
US-10-330-613A-51
; Sequence 51, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-51

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
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Qy 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSDP 95
Db 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSYP 95

RESULT 9
US-10-330-613A-52
; Sequence 52, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-52

Query Match      86.2%; Score 481; DB 2; Length 95;
Best Local Similarity 97.9%; Pred. No. 9.3e-38;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGIIRNDLQWYQKPGKAPKRLIYAASSLSQGVPS 60

Qy 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSDP 95
Db 61 RFSGSGGTDTFTLTISLQPEDPATYTCLOHNSYP 95

RESULT 10
US-08-599-226-9
; Sequence 9, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
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/ FILING DATE: 08-FEB-1996
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeConti, Giulio A., Jr.
/ REGISTRATION NUMBER: 31,503
/ REFERENCE/DOCKET NUMBER: BBI-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ US-08-599-226-9

Query Match      86.2%; Score 481; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKNSAPYAFGGTKVEIK 107
Db 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKNSAPYAFGGTKVEIK 107

RESULT 11
US-09-125-098-9
; Sequence 9, Application US/09125098
; Patent No. 6258562
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; INFORMATION FOR SEQ ID NO: 9:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
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/ REFERENCE/DOCKET NUMBER: BBI-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ US-09-125-098-9

Query Match      86.2%; Score 481; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASLSQGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKNSAPYAFGGTKVEIK 107
Db 61 RFGSGSGTDFLTITSSLOPEDVATYYCQKNSAPYAFGGTKVEIK 107

RESULT 12
US-09-540-018-9
; Sequence 9, Application US/09540018
; Patent No. 6509015
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/540,018
; FILING DATE: 31-MARCH-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-540-018-9

Query Match      86.2%; Score 481; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.1e-37;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTKEIR 107

RESULT 13
US-09-025-769B-28
; Sequence 28, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-28

Query Match      86.0%; Score 480; DB 2; Length 109;
Best Local Similarity 87.9%; Pred. No. 1.3e-37;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTKEIR 107

RESULT 14
US-09-025-769B-43
; Sequence 43, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: EP 95 11 3021.0
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-43

Query Match      86.0%; Score 480; DB 2; Length 109;
Best Local Similarity 87.9%; Pred. No. 1.3e-37;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCLOHNSDPCSFQGTKEIR 107

RESULT 15
US-09-490-070A-28
; Sequence 28, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
```

Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Colin G. Sandercock, Esq. c/o Heller Ehrman
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA: US/09/490,070A
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 US-09-490-070A-28

Query Match 86.0%; Score 480; DB 2; Length 109;
 Best Local Similarity 87.9%; Pred. No. 1.3e-37;
 Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLGWYQKPKAPKLLIYAASSLSQGVPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISSYLAWYQKPKAPKLLIYAASSLSQGVPS 60
 QY 61 RFSGSGSGTDFTLTISSLQPEDFATYYCLOHNSDPCSFQGGTKLEIR 107
 Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQGHYTPPTFGGTTKVEIK 107

Search completed: April 25, 2007, 04:08:29
 Job time : 14.4506 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 40 Seconds
(without alignments)
1251.741 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQMTSPSLASVGDVRT.....CLQHNSDPCSFQGTGLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	100.0	107	4	US-10-041-860-22
2	558	100.0	107	4	US-10-041-860-227
3	558	100.0	107	4	US-10-041-860-261
4	558	100.0	107	4	US-10-041-860-262
5	558	100.0	107	4	US-10-041-860-297
6	558	100.0	107	4	US-10-665-383-24
7	542	97.1	107	4	US-10-684-109-53
8	542	97.1	234	4	US-10-684-109-109
9	539	96.6	107	4	US-10-684-109-41
10	539	96.6	234	4	US-10-684-109-91
11	528	94.6	107	4	US-10-041-860-265
12	528	94.6	236	4	US-10-038-591-48
13	528	94.6	236	4	US-10-775-444A-48
14	528	94.6	236	6	US-11-144-248-48
15	528	94.6	236	6	US-11-144-248-48
16	528	94.6	236	6	US-11-182-343-48
17	527	94.4	108	5	US-10-805-177-68
18	527	94.4	108	5	US-10-805-177-72
19	525	94.1	107	4	US-10-330-613-18
20	525	94.1	107	4	US-10-330-530-18
21	525	94.1	107	4	US-10-041-860-26
22	525	94.1	107	4	US-10-041-860-28
23	525	94.1	107	4	US-10-041-860-36
24	525	94.1	107	4	US-10-041-860-231
25	525	94.1	107	4	US-10-041-860-232
26	525	94.1	107	4	US-10-041-860-234
27	525	94.1	107	4	US-10-041-860-266

28	525	94.1	107	4	US-10-041-860-268
29	525	94.1	107	4	US-10-041-860-316
30	525	94.1	107	4	US-10-041-860-340
31	525	94.1	107	4	US-10-309-762-166
32	525	94.1	107	4	US-10-660-357-18
33	525	94.1	107	4	US-10-665-383-32
34	525	94.1	107	4	US-10-665-383-36
35	525	94.1	107	4	US-10-665-383-52
36	525	94.1	107	5	US-10-727-155-274
37	525	94.1	107	5	US-10-727-155-307
38	525	94.1	236	4	US-10-038-591-52
39	525	94.1	236	4	US-10-775-444A-52
40	525	94.1	236	5	US-10-917-073A-6
41	525	94.1	236	6	US-11-144-248-52
42	525	94.1	236	6	US-11-144-222-52
43	525	94.1	236	6	US-11-182-343-52
44	524	93.9	107	5	US-10-727-155-60
45	524	93.9	107	5	US-10-822-306A-16

ALIGNMENTS

RESULT 1

US-10-041-860-22
; Sequence 22, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-22

Query Match 100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIQMTSPSLASVGDVRTITCRASGIRNDLGWYQKFKAPKRLIYAASSLSQSGVPS	60
Db	1	DIQMTSPSLASVGDVRTITCRASGIRNDLGWYQKFKAPKRLIYAASSLSQSGVPS	60
QY	61	RFSGSGSGDTFTITISLQPEDFATYYCLQHNSDPCSFQGTGLEIR	107
Db	61	RFSGSGSGDTFTITISLQPEDFATYYCLQHNSDPCSFQGTGLEIR	107

RESULT 2

US-10-041-860-227
; Sequence 227, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi

```
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 227
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-227

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 3
US-10-041-860-261
; Sequence 261, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-261

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 4
US-10-041-860-262
; Sequence 262, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
```

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; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-262

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 5
US-10-041-860-297
; Sequence 297, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-297

Query Match          100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVSGDRVTITCRASQGIIRNDLWYQKPKGKAPKRLIYAASSLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTITSSLPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 6
US-10-041-860-297
```

```
US-10-665-383-24
; Sequence 24, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gad
; APPLICANT: Keyt, Bruce
; APPLICANT: Laroche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PGPF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX-052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; PRIOR FILING DATE: 2003-09-16
; PRIOR FILING DATE: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-24

Query Match      100.0%; Score 558; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107

RESULT 7
US-10-684-109-53
; Sequence 53, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR FILING DATE: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-53

Query Match      97.1%; Score 542; DB 4; Length 107;
Best Local Similarity 97.2%; Pred. No. 3.1e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107

US-10-684-109-109
; Sequence 109, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR FILING DATE: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-109

Query Match      97.1%; Score 542; DB 4; Length 234;
Best Local Similarity 97.2%; Pred. No. 6.5e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 21 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 80

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 107
Db 81 RFGSGSGTDFLTITSSLOPEDFATYYCLOHNSDPCSFQGTGLEIR 127

RESULT 9
US-10-684-109-41
; Sequence 41, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR FILING DATE: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-41

Query Match      96.6%; Score 539; DB 4; Length 107;
Best Local Similarity 96.3%; Pred. No. 5.5e-39;
Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIGIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
```


RESULT 15
US-11-144-222-48
; Sequence 48, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 41 Seconds
(without alignments)
533.620 Million cell updates/sec

Title: US-10-665-383-24

Perfect score: 558

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQNSDPCSFQGTGLEIR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New.*
- 1: /EMC_Celerra_SID33/ptodata/1/pubpaa/US08_NEW_PUB.pdb.*
 - 2: /EMC_Celerra_SID33/ptodata/1/pubpaa/US06_NEW_PUB.pdb.*
 - 3: /EMC_Celerra_SID33/ptodata/1/pubpaa/US07_NEW_PUB.pdb.*
 - 4: /EMC_Celerra_SID33/ptodata/1/pubpaa/PCT_NEW_PUB.pdb.*
 - 5: /EMC_Celerra_SID33/ptodata/1/pubpaa/US09_NEW_PUB.pdb.*
 - 6: /EMC_Celerra_SID33/ptodata/1/pubpaa/US10_NEW_PUB.pdb.*
 - 7: /EMC_Celerra_SID33/ptodata/1/pubpaa/US11_NEW_PUB.pdb.*
 - 8: /EMC_Celerra_SID33/ptodata/1/pubpaa/US60_NEW_PUB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	558	100.0	107	7	US-11-109-181-22
2	558	100.0	107	7	US-11-109-181-227
3	558	100.0	107	7	US-11-109-181-261
4	558	100.0	107	7	US-11-109-181-262
5	558	100.0	107	7	US-11-109-181-297
6	542	97.1	107	7	US-11-433-924-384
7	535	95.9	107	7	US-11-433-924-376
8	528	94.6	107	7	US-11-109-181-265
9	528	94.6	108	6	US-10-515-149-39
10	528	94.6	108	7	US-11-346-403A-61
11	528	94.6	236	7	US-11-290-687-27
12	528	94.6	236	7	US-11-404-967-27
13	525	94.1	107	7	US-11-239-308-8
14	525	94.1	107	7	US-11-479-339-18
15	525	94.1	107	7	US-11-109-181-26
16	525	94.1	107	7	US-11-109-181-28
17	525	94.1	107	7	US-11-109-181-36
18	525	94.1	107	7	US-11-109-181-231
19	525	94.1	107	7	US-11-109-181-232
20	525	94.1	107	7	US-11-109-181-234
21	525	94.1	107	7	US-11-109-181-266
22	525	94.1	107	7	US-11-109-181-268
23	525	94.1	107	7	US-11-109-181-316
24	525	94.1	107	7	US-11-109-181-340
25	525	94.1	108	7	US-11-311-939-95

ALIGNMENTS

RESULT 1

US-11-109-181-22

; Sequence 22, Application US/11109181

; Publication No. US20060293506A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Peng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadi

; APPLICANT: Weber, Richard

; APPLICANT: Bezaheh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGPD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/11/109,181

; PRIOR FILING DATE: 2005-04-18

; PRIOR APPLICATION NUMBER: US/10/041,860

; PRIOR FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22

; LENGTH: 107

; TYPE: PRT

; ORGANISM: homo sapiens

US-11-109-181-22

Query Match 100.0%; Score 558; DB 7; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.5e-44;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGIKNDLWYQKPKAPKRLIYAASSLSQGVPS 60

QY 61 RFGSGSGTDTFTITSLQPEDFATYTCLOHNSDPCSFQGTGLEIR 107

Db 61 RFGSGSGTDTFTITSLQPEDFATYTCLOHNSDPCSFQGTGLEIR 107

RESULT 2

US-11-109-181-227

; Sequence 227, Application US/11109181

; Publication No. US20060293506A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

Sequence 25, Appl
Sequence 25, Appl
Sequence 9, Appl
Sequence 181, App
Sequence 637, App
Sequence 348, App
Sequence 127, App
Sequence 113, App
Sequence 149, App
Sequence 20, Appl
Sequence 20, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 233, App
Sequence 267, App
Sequence 285, App
Sequence 636, App
Sequence 67, Appl

26 525 94.1 236 7 US-11-290-687-25
27 525 94.1 236 7 US-11-404-967-25
28 525 93.9 108 7 US-11-311-939-9
29 524 93.9 108 7 US-11-311-939-181
30 524 93.9 108 7 US-11-311-939-637
31 522 93.5 107 7 US-11-433-924-348
32 522 93.5 108 7 US-11-311-939-113
33 522 93.5 108 7 US-11-311-939-127
34 522 93.5 108 7 US-11-311-939-149
35 521 93.4 107 7 US-11-290-687-20
36 521 93.4 107 7 US-11-404-967-20
37 521 93.4 236 7 US-11-290-687-28
38 521 93.4 236 7 US-11-404-967-28
39 519 93.0 107 7 US-11-479-339-14
40 519 93.0 107 7 US-11-109-181-18
41 519 93.0 107 7 US-11-109-181-233
42 519 93.0 107 7 US-11-109-181-267
43 519 93.0 107 7 US-11-109-181-285
44 518 92.8 106 7 US-11-311-939-636
45 518 92.8 107 7 US-11-410-886-67

```

; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 227
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-227

Query Match          100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107

RESULT 3
US-11-109-181-261
; Sequence 261, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-261

Query Match          100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107

RESULT 4
US-11-109-181-262
; Sequence 262, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-262

Query Match          100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60
Db 1 DIQMTSPSSLSASVSGDRVTITCRASQGIKNDLWYQKPGKAPKRLIYAASSLSQSGVPS 60

QY 61 RFSGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICLQHNSDPCSFQGGTKLEIR 107

RESULT 5
US-11-109-181-297
; Sequence 297, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-297

Query Match          100.0%; Score 558; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
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```
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 6
US-11-433-924-384
; Sequence 384, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Aimee
; APPLICANT: Foord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-384

Query Match 97.1%; Score 542; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 4.6e-43;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 7
US-11-433-924-376
; Sequence 376, Application US/11433924
; Publication No. US20060286112A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Aimee
; APPLICANT: Foord, Orit
; APPLICANT: Belouski, Shelley Sims
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES THAT BIND TO
; TITLE OF INVENTION: VERY LATE ANTIGEN-1 FOR THE TREATMENT OF INFLAMMATION AND
; TITLE OF INVENTION: OTHER DISORDERS
; FILE REFERENCE: ABGENIX.120A
; CURRENT APPLICATION NUMBER: US/11/433,924
; CURRENT FILING DATE: 2006-05-12
; PRIOR APPLICATION NUMBER: US 60/681,846
; PRIOR FILING DATE: 2005-05-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-433-924-376
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```
Query Match 95.9%; Score 535; DB 7; Length 107;
Best Local Similarity 95.3%; Pred. No. 2.1e-42;
Matches 102; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 8
US-11-109-181-265
; Sequence 265, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R. F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-265

Query Match 94.6%; Score 528; DB 7; Length 107;
Best Local Similarity 95.3%; Pred. No. 9.2e-42;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQWTSPLSASVSGDRVTITCRASQGIIRNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Qy 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107
Db 61 RFGSGSGTDFTLTITSSLOPEDPATYCYCLOHNSDPCSFQGGTKLEIR 107

RESULT 9
US-10-515-149-39
; Sequence 39, Application US/10515149
; Publication No. US20060194276A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna
; APPLICANT: Krauss, Juergen
; APPLICANT: Arndt, Michaela
; APPLICANT: Martin, Andrew C. R.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: University of Reading
; TITLE OF INVENTION: Specificity Framework
; TITLE OF INVENTION: Framework
; FILE REFERENCE: 015280-459100US
; CURRENT APPLICATION NUMBER: US/10/515,149
; CURRENT FILING DATE: 2004-11-18
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; PRIOR APPLICATION NUMBER: US 60/390,033
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: WO PCT/US03/19333
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human V-L germline sequence
US-10-515-149-39

Query Match 94.6%; Score 528; DB 6; Length 108;
Best Local Similarity 95.3%; Pred. No. 9.3e-42;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 107
Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 107

RESULT 10
US-11-346-403A-61
; Sequence 61, Application US/11346403A
; Publication No. US20060234302A1
; GENERAL INFORMATION:
; APPLICANT: Hoet, Rene
; APPLICANT: Schoonbroodt, Sonia
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: LIBRARIES AND METHODS FOR
; TITLE OF INVENTION: ISOLATING ANTIBODIES
; FILE REFERENCE: 10280-116001
; CURRENT APPLICATION NUMBER: US/11/346,403A
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: US 60/649,065
; PRIOR FILING DATE: 2005-02-01
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-346-403A-61

Query Match 94.6%; Score 528; DB 7; Length 108;
Best Local Similarity 95.3%; Pred. No. 9.3e-42;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 2 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 61
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 107
Db 62 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 108

RESULT 11
US-11-290-687-27
; Sequence 27, Application US/11290687
; Publication No. US20060140960A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Yan
; APPLICANT: Pachter, Jonathan
; APPLICANT: Wang, Yaolin

; APPLICANT: Liu, Ming
; TITLE OF INVENTION: BIOMARKERS FOR PRE-SELECTION OF PATIENTS FOR ANTI-IGF1R THERAPY
; FILE REFERENCE: JB06257 US01
; CURRENT APPLICATION NUMBER: US/11/290,687
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: 60/633,156
; PRIOR FILING DATE: 2004-12-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain immunoglobulin
US-11-290-687-27

Query Match 94.6%; Score 528; DB 7; Length 236;
Best Local Similarity 95.3%; Pred. No. 2.1e-41;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 82
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 107
Db 83 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 129

RESULT 12
US-11-404-967-27
; Sequence 27, Application US/11404967
; Publication No. US20060233810A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Yaolin
; APPLICANT: Liu, Ming
; APPLICANT: Wang, Yan
; APPLICANT: Pachter, Jonathan A
; APPLICANT: Bishop, Walter R
; TITLE OF INVENTION: Methods and Compositions for Treating or Preventing Cancer
; FILE REFERENCE: OC06331 US
; CURRENT APPLICATION NUMBER: US/11/404,967
; CURRENT FILING DATE: 2006-04-14
; PRIOR APPLICATION NUMBER: 60/671,654
; PRIOR FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain immunoglobulin
US-11-404-967-27

Query Match 94.6%; Score 528; DB 7; Length 236;
Best Local Similarity 95.3%; Pred. No. 2.1e-41;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 60
Db 23 DIQMTQSPSSLSASVGDRTVITCRASQGI RNDLGWYQKPGKAPKRLIYAASSLSQGVPS 82
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 107
Db 83 RFGSGSGTDFLTITSSLOPEDFATYYCLQHNSDPCSFQGTGLEIR 129

RESULT 13
US-11-239-308-8
; Sequence 8, Application US/11239308
; Publication No. US20060088883A1

```

; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-8

Query Match          94.1%; Score 525; DB 7; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.8e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDTLTITSSQLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTLTITSSQLQPEDFATYYCLOHNSYPWTFQGTKEIK 107

RESULT 14
US-11-479-339-18
; Sequence 18, Application US/11479339
; Publication No. US20060246077A1
; GENERAL INFORMATION:
; APPLICANT: Menashe, Bar-El
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ARGENIX.030C2
; CURRENT APPLICATION NUMBER: US/11/479,339
; CURRENT FILING DATE: 2006-06-30
; PRIOR APPLICATION NUMBER: 10/660,357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346,460
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-479-339-18

Query Match          94.1%; Score 525; DB 7; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.8e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDTLTITSSQLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTLTITSSQLQPEDFATYYCLOHNSYPWTFQGTKEIK 107

RESULT 15
US-11-109-181-26
; Sequence 26, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-26

Query Match          94.1%; Score 525; DB 7; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.8e-41;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQIRNDLGWYQKPKAPKRLIYAASSLSQGVPS 60

Qy 61 RFGSGSGTDTLTITSSQLQPEDFATYYCLOHNSDPCSFQGTKEIR 107
Db 61 RFGSGSGTDTLTITSSQLQPEDFATYYCLOHNSYPWTFQGTKEIK 107

Search completed: April 25, 2007, 04:27:43
Job time : 41.2585 secs
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 112 Seconds
(without alignments)
564.248 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVQLVQSGAEVKPGESLKI.....YYHHGMDVWGQGTITVTVSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_200701.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*
- 11: Geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699	100.0	129	7	ADK18605
2	699	100.0	129	7	ADK18791
3	699	100.0	129	7	ADK18895
4	699	100.0	129	7	ADK18826
5	699	100.0	129	8	ADL25428
6	623	89.1	474	9	AEA12652
7	623	89.1	474	9	AEA12653
8	623	89.1	474	9	AEA18909
9	623	89.1	474	9	AEA18908
10	623	89.1	474	9	AEA18548
11	623	89.1	474	9	AEA18549
12	623	89.1	474	9	AEA10642
13	623	89.1	474	9	AEA10641
14	623	89.1	474	9	AEA125714
15	623	89.1	474	9	AEA125715
16	623	89.1	474	9	AEA125716
17	623	89.1	474	9	AEA125717
18	623	89.1	474	9	AEA125718
19	623	89.1	474	9	AEA125719
20	603	86.3	125	9	ADY26764
21	598.5	85.6	126	7	ADK18889
22	593.5	84.9	126	7	ADK18603

23	593.5	84.9	126	7	ADK18790	Adk18790 Anti-huma
24	593.5	84.9	126	7	ADK18825	Adk18825 Anti-huma
25	593.5	84.9	126	8	ADL25424	Adl25424 Human mAb
26	592.5	84.8	126	7	ADK18876	Adk18876 Anti-huma
27	592.5	84.8	126	7	ADK18599	Adk18599 Anti-huma
28	592.5	84.8	126	7	ADK18824	Adk18824 Anti-huma
29	592.5	84.8	126	8	ADL25416	Adl25416 Human mAb
30	592	84.7	156	10	AEK98291	Aek98291 Human 161
31	592	84.7	156	10	AEK98296	Aek98296 Human 161
32	592	84.7	182	10	AEK98221	Aek98221 Human 161
33	592	84.7	182	10	AEK98278	Aek98278 Human 161
34	590	84.4	118	8	ADP47228	Adp47228 Human pho
35	590	84.4	178	10	AEK98274	Aek98274 Human 161
36	590	84.4	178	10	AEK98213	Aek98213 Human 161
37	589.5	84.3	126	7	ADK18611	Adk18611 Anti-huma
38	589.5	84.3	126	7	ADK18792	Adk18792 Anti-huma
39	589.5	84.3	126	7	ADK18913	Adk18913 Anti-huma
40	589.5	84.3	126	8	ADL25440	Adl25440 Human mAb
41	589.5	84.3	126	8	ADP47088	Adp47088 Human pho
42	587	84.0	118	8	ADP47224	Adp47224 Human pho
43	585	83.7	118	8	ADP47225	Adp47225 Human pho
44	584	83.5	118	8	ADP47225	Adp47225 Human pho
45	584	83.5	118	8	ADP47098	Adp47098 Human pho

ALIGNMENTS

RESULT 1
ADK18605
ID ADK18605 standard; protein; 129 AA.
AC ADK18605;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody heavy chain protein sequence.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
XX Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
XX Bezabeh B;
XX WPI; 2003-587119/55.
XX
XX New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX
XX Disclosure; SEQ ID NO 29; 255pp; English.
XX
XX The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.

```
XX SQ Sequence 129 AA;
Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSWIGVWRQMPGKGLWMMGIIYPGDS DTRY 60
DQ |||||
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSWIGVWRQMPGKGLWMMGIIYPGDS DTRY 60
QY 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
DQ |||||
DB 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
QY 121 QGTTVTSS 129
DQ |||||
DB 121 QGTTVTSS 129

RESULT 2
ADK18791
ID ADK18791 standard; protein; 129 AA.
XX AC ADK18791;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-human PDGF-D antibody protein related sequence #17.
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX OS Homo sapiens.
XX PN WO2003057857-A2.
XX PD 17-JUL-2003.
XX PF 06-JAN-2003; 2003WO-US000398.
XX PR 07-JAN-2002; 2002US-00041860.
XX PA (ABGE-) ABGENIX INC.
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX DR New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX PS Disclosure; SEQ ID NO 215; 255pp; English.
XX CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX SQ Sequence 129 AA;
Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSWIGVWRQMPGKGLWMMGIIYPGDS DTRY 60
DQ |||||
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSWIGVWRQMPGKGLWMMGIIYPGDS DTRY 60
QY 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
DQ |||||
DB 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
QY 121 QGTTVTSS 129
DQ |||||
DB 121 QGTTVTSS 129

RESULT 3
ADK18895
ID ADK18895 standard; protein; 129 AA.
XX AC ADK18895;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-human PDGF-D antibody protein related sequence #121.
XX KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX OS Homo sapiens.
XX PN WO2003057857-A2.
XX PD 17-JUL-2003.
XX PF 06-JAN-2003; 2003WO-US000398.
XX PR 07-JAN-2002; 2002US-00041860.
XX PA (ABGE-) ABGENIX INC.
XX PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX WPI; 2003-587119/55.
XX DR New human monoclonal antibody that binds to platelet-derived growth
XX factor-D (PDGF-D), useful for treating chronic and recurrent human
XX diseases, such as inflammation, autoimmunity and cancer.
XX PS Disclosure; SEQ ID NO 319; 255pp; English.
XX CC The invention relates to a human monoclonal antibody that binds to
XX platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
XX treating chronic and recurrent human diseases, such as inflammation,
XX autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
XX useful for modulating collagen formation, and for staging various
XX cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
XX generated using an active protein fragment of the gene product from the
XX clone 30664188.0.99 arising in the conditioned medium obtained when
XX HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
XX sequence corresponds to a protein used in the invention.
XX SQ Sequence 129 AA;
Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSWIGVWRQMPGKGLWMMGIIYPGDS DTRY 60
DQ |||||
DB 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSWIGVWRQMPGKGLWMMGIIYPGDS DTRY 60
QY 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
DQ |||||
DB 61 SPSPFQQTATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVVGATIGGYYHHGMDVWG 120
QY 121 QGTTVTSS 129
DQ |||||
DB 121 QGTTVTSS 129
```



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Db      121 QGTTVTSS 129
|||||
RESULT 4
ADK18826
ID ADK18826 standard; protein; 129 AA.
XX
AC ADK18826;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #52.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 250; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 129 AA;

Query Match      100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPKGLWNGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVDWG 120
DB 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVDWG 120
QY 121 QGTTVTSS 129
DB 121 QGTTVTSS 129

RESULT 5
ADL25428
ID ADL25428 standard; protein; 129 AA.
XX
AC ADL25428;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human mAb 1.29 heavy chain variable region protein SEQ ID NO:38.
XX
KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW gene therapy; human; monoclonal antibody; mAb.
XX
OS Homo sapiens.
XX
PN WO2004024098-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029414.
XX
PR 16-SEP-2002; 2002US-0411137P.
XX
PA (ABGE-) ABGENIX INC.
PA (CURA-) CURAGEN CORP.
XX
PI Floege J, Gazit-Bornstein G, Keyt B, Larochele WJ, Lichenstein H;
PI N-PSDB; ADL25427.
XX
DR WPI; 2004-269881/25.
XX
PT Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.
XX
PS Disclosure; SEQ ID NO 38; 115pp; English.
XX
CC The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 129 AA;

Query Match      100.0%; Score 699; DB 8; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPKGLWNGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPQESLKISKKGSGYFTSYWIGVRQMPKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVDWG 120
DB 61 SPSPGQATISADKSIATYLOWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVDWG 120
QY 121 QGTTVTSS 129
DB 121 QGTTVTSS 129

RESULT 6
ADL2652
ID ADL2652 standard; protein; 474 AA.
XX

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AC AEA12652;
 XX 28-JUL-2005 (first entry)
 XX Heavy chain of CHIR-5.9 human anti-CD40 antibody.
 DE cancer; B-cell; antibody therapy; CD40; CD20; tumor; cytostatic;
 XX b-cell acute lymphoblastic leukemia; b-cell lymphoma; heavy chain.
 KW Homo sapiens.
 XX WO2005044307-A2.
 XX 19-MAY-2005.
 XX 04-NOV-2004; 2004WO-US037159.
 XX 04-NOV-2003; 2003US-0517337P.
 PR 26-NOV-2003; 2003US-0525579P.
 PR 27-APR-2004; 2004US-0565710P.
 PR 28-SEP-2004; 2004US-0613885P.
 XX (CHIR) CHIRON CORP.
 PA Long L, Luqman M, Yabannavar A, Zaror I;
 XX WPI; 2005-346957/35.
 XX Treating human subjects for B cell-related cancers (e.g. multiple myeloma
 PT of Burkitt's lymphoma) comprises administering to the subject an amount
 PT of an antagonist anti-CD40 antibody in combination with an anti-CD20
 PT antibody.
 XX Claim 1; SEQ ID NO 7; 133pp; English.
 XX The invention relates to a novel method for treating a human subject for
 CC a cancer characterized by neoplastic B cell growth. The method comprises
 CC administering to the subject combination antibody therapy, which
 CC comprises an amount of an anti-CD40 antibody or its antigen-binding
 CC fragment in combination with an anti-CD20 antibody or its antigen-binding
 CC fragment, where the anti-CD40 antibody or antigen-binding fragment is
 CC free of significant agonist activity when bound to the CD40 antigen. The
 CC invention further comprises: methods of inhibiting the growth of a tumor
 CC comprising neoplastic B cells. The methods and compositions have
 CC cytostatic activity. The methods are useful for treating B cell-related
 CC cancer (e.g. lymphoma or leukemia) or in manufacturing medicaments for
 CC the treatment of such a disease. This sequence represents a heavy chain
 CC of CHIR-5.9 human anti-CD40 antibody of the invention.
 XX Sequence 474 AA;
 SQ
 Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPESLKISKSGSYFTSWIGVWRQMPGKGLWNGIYPGSDTRY 60
 DB 20 EVQLVQSGAEVKKPESLKISKSGSYFTSWIGVWRQMPGKGLWNGIYPGSDTRY 79
 QY 61 SPSPGQATISADKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVG 120
 DB 80 SPSPGQVTTISADKSTAYLQWSSLKASDTAMYCAR-----GTAAGRDYHYHYHGMVDVG 135
 QY 121 QGTTVTSS 129
 DB 136 QGTTVTSS 144
 RESULT 7
 AEA12653
 ID AEA12653 standard; protein; 474 AA.
 XX AEA12653;
 AC

XX 28-JUL-2005 (first entry)
 XX Heavy chain variant of CHIR-5.9 human anti-CD40 antibody.
 DE cancer; B-cell; antibody therapy; CD40; CD20; tumor; cytostatic;
 KW b-cell acute lymphoblastic leukemia; b-cell lymphoma; heavy chain;
 KW munitin.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2005044307-A2.
 XX 19-MAY-2005.
 XX 04-NOV-2004; 2004WO-US037159.
 XX 04-NOV-2003; 2003US-0517337P.
 PR 26-NOV-2003; 2003US-0525579P.
 PR 27-APR-2004; 2004US-0565710P.
 PR 28-SEP-2004; 2004US-0613885P.
 XX (CHIR) CHIRON CORP.
 PA Long L, Luqman M, Yabannavar A, Zaror I;
 XX WPI; 2005-346957/35.
 XX Treating human subjects for B cell-related cancers (e.g. multiple myeloma
 PT of Burkitt's lymphoma) comprises administering to the subject an amount
 PT of an antagonist anti-CD40 antibody in combination with an anti-CD20
 PT antibody.
 XX Claim 1; SEQ ID NO 8; 133pp; English.
 XX The invention relates to a novel method for treating a human subject for
 CC a cancer characterized by neoplastic B cell growth. The method comprises
 CC administering to the subject combination antibody therapy, which
 CC comprises an amount of an anti-CD40 antibody or its antigen-binding
 CC fragment in combination with an anti-CD20 antibody or its antigen-binding
 CC fragment, where the anti-CD40 antibody or antigen-binding fragment is
 CC free of significant agonist activity when bound to the CD40 antigen. The
 CC invention further comprises: methods of inhibiting the growth of a tumor
 CC comprising neoplastic B cells. The methods and compositions have
 CC cytostatic activity. The methods are useful for treating B cell-related
 CC cancer (e.g. lymphoma or leukemia) or in manufacturing medicaments for
 CC the treatment of such a disease. This sequence represents a heavy chain
 CC variant of a CHIR-5.9 human anti-CD40 antibody of the invention.
 XX Sequence 474 AA;
 SQ
 Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPESLKISKSGSYFTSWIGVWRQMPGKGLWNGIYPGSDTRY 60
 DB 20 EVQLVQSGAEVKKPESLKISKSGSYFTSWIGVWRQMPGKGLWNGIYPGSDTRY 79
 QY 61 SPSPGQATISADKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVG 120
 DB 80 SPSPGQVTTISADKSTAYLQWSSLKASDTAMYCAR-----GTAAGRDYHYHYHGMVDVG 135
 QY 121 QGTTVTSS 129
 DB 136 QGTTVTSS 144
 RESULT 8
 AEA18909
 ID AEA18909 standard; protein; 474 AA.
 XX

AC AEA18908;
 XX 28-JUL-2005 (first entry)
 DE Variant heavy chain of CHIR-5.9 human anti-CD40 antibody.
 DE chronic lymphocytic leukemia; CLL; anti-CD40 antibody; CD40; CHIR-5.9;
 DE CHIR-12.12; antibody therapy; heavy chain.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX Peptide 1..19
 XX /note= "leader peptide"
 PN Region 20..144
 XX /note= "variable region"
 XX Region 145..474
 XX /note= "constant region"
 XX WO2005044304-A2.
 XX 19-MAY-2005.
 XX 04-NOV-2004; 2004WO-US036954.
 XX 04-NOV-2003; 2003US-0517337P.
 PR 26-NOV-2003; 2003US-0525579P.
 PR 27-APR-2004; 2004US-0565710P.
 PR 21-SEP-2004; 2004US-0611794P.
 XX (CHIR) CHIRON CORP.
 PA Long L, Luqman M, Yabannavar A, Zaror I, Aukerman L;
 PI WPI; 2005-346955/35.
 XX Treating human subjects for chronic lymphocytic leukemia comprises
 PT administering to the subject an amount of a human antagonist anti-CD40
 PT monoclonal antibody that specifically binds to the CD40 antigen.
 XX Claim 1; SEQ ID NO 8; 115pp; English.
 XX The specification describes a method of treating a human subject for
 CC chronic lymphocytic leukemia (CLL). The method comprises administering an
 CC amount of a human anti-CD40 monoclonal antibody that specifically binds
 CC to a human CD40 antigen expressed on the surface of a human CD40-
 CC expressing cell and is free of significant agonist activity, where when
 CC the antibody binds to the CD40 antigen expressed on the surface of the
 CC cell, the growth or differentiation of the cell is inhibited. The human
 CC anti-CD40 monoclonal antibody is selected from CHIR-5.9 or CHIR-12.12.
 CC The method of the invention is useful for treating chronic lymphocytic
 CC leukemia or in manufacturing medicaments for the treatment of such
 CC diseases. The present sequence represents a variant heavy chain of human
 CC anti-CD40 monoclonal antibody CHIR-5.9.
 XX Sequence 474 AA;
 SQ Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVROMPGKLEWMGIYPGSDTRY 60
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVROMPGKLEWMGIYPGSDTRY 79
 QY 61 SPSFQQTISADKSIISTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120
 DB 80 SPSFQQTISADKSIISTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 135
 QY 121 QGTTVTSS 129
 DB 136 QGTTVTSS 144
 RESULT 9
 AEA18908
 ID AEA18908 standard; protein; 474 AA.
 XX AEA18908;
 AC AEA18908;
 XX 28-JUL-2005 (first entry)

XX Heavy chain of CHIR-5.9 human anti-CD40 antibody.
 DE chronic lymphocytic leukemia; CLL; anti-CD40 antibody; CD40; CHIR-5.9;
 KW CHIR-12.12; antibody therapy; heavy chain.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX Peptide 1..19
 XX /note= "leader peptide"
 FT Region 20..144
 FT /note= "variable region"
 FT Region 145..474
 FT /note= "constant region"
 XX WO2005044304-A2.
 XX 19-MAY-2005.
 XX 04-NOV-2004; 2004WO-US036954.
 XX 04-NOV-2003; 2003US-0517337P.
 PR 26-NOV-2003; 2003US-0525579P.
 PR 27-APR-2004; 2004US-0565710P.
 PR 21-SEP-2004; 2004US-0611794P.
 XX (CHIR) CHIRON CORP.
 PA Long L, Luqman M, Yabannavar A, Zaror I, Aukerman L;
 PI WPI; 2005-346955/35.
 XX Treating human subjects for chronic lymphocytic leukemia comprises
 PT administering to the subject an amount of a human antagonist anti-CD40
 PT monoclonal antibody that specifically binds to the CD40 antigen.
 XX Claim 1; SEQ ID NO 7; 115pp; English.
 XX The specification describes a method of treating a human subject for
 CC chronic lymphocytic leukemia (CLL). The method comprises administering an
 CC amount of a human anti-CD40 monoclonal antibody that specifically binds
 CC to a human CD40 antigen expressed on the surface of a human CD40-
 CC expressing cell and is free of significant agonist activity, where when
 CC the antibody binds to the CD40 antigen expressed on the surface of the
 CC cell, the growth or differentiation of the cell is inhibited. The human
 CC anti-CD40 monoclonal antibody is selected from CHIR-5.9 or CHIR-12.12.
 CC The method of the invention is useful for treating chronic lymphocytic
 CC leukemia or in manufacturing medicaments for the treatment of such
 CC diseases. The present sequence represents the heavy chain of human anti-
 CC CD40 monoclonal antibody CHIR-5.9.
 XX Sequence 474 AA;
 SQ Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVROMPGKLEWMGIYPGSDTRY 60
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVROMPGKLEWMGIYPGSDTRY 79
 QY 61 SPSFQQTISADKSIISTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120
 DB 80 SPSFQQTISADKSIISTAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 135
 QY 121 QGTTVTSS 129
 DB 136 QGTTVTSS 144
 RESULT 10
 AEA18548

ID AEA18548 standard; protein; 474 AA.
 AC AEA18548;
 XX
 DT 28-JUL-2005 (first entry)
 DE Heavy chain of anti-CD40 antibody CHIR-5.9.
 KW cytostatic; gene therapy; neoplasm; solid tumor; CD40; heavy chain;
 KW antibody CHIR-5.9; antibody therapy; ss.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19 /note= "leader peptide"
 FT Region 20..144 /note= "variable region"
 FT Region 145..474 /note= "constant region"
 FT
 FT
 PN WO2005044305-A2.
 XX
 PD 19-MAY-2005.
 XX
 PF 04-NOV-2004; 2004WO-US036955.
 XX
 PR 04-NOV-2003; 2003US-0517337P.
 PR 26-NOV-2003; 2003US-0525579P.
 PR 27-APR-2004; 2004US-0565634P.
 PR 27-APR-2004; 2004US-0565710P.
 XX
 PA (CHIR) CHIRON CORP.
 PI Long L, Luqman M, Yabannavar A, Zaror I;
 XX
 DR WPI; 2005-346956/35.
 XX
 XX Treating human subjects for solid tumors that express CD40 cell-surface antigen comprises administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the CD40 antigen.
 XX
 PS Claim 1; SEQ ID NO 7; 123pp; English.
 XX
 CC The specification describes a method of treating a human subject for a solid tumor comprising carcinoma cells expressing CD40 antigen. The method comprises administering to the subject an amount of a human anti-CD40 monoclonal antibody that is capable of specifically binding to the CD40 antigen, the monoclonal antibody being free of significant agonist activity when bound to CD40 antigen. The method of the invention is useful for treating solid tumors expressing the CD40 cell-surface antigen, such as sarcomas or carcinoma of the lungs, breasts, ovary, skin, colon or urinary bladder, or in manufacturing medicaments for the treatment of such diseases. The present sequence represents the heavy chain of anti-CD40 monoclonal antibody CHIR-5.9. This antibody represents an antibody which can be used in the method of the invention.
 XX
 SQ Sequence 474 AA;
 Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVWRMPGKGLWGMGIYPGSDSTRY 60
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVWRMPGKGLWGMGIYPGSDSTRY 79
 QY 61 SPSPGQQTATISADKSIATYLOWSSLSKASDTAMTYCARHVDVGATIGGYYHYHGMVDWG 120
 DB 80 SPSPGQQTATISADKSIATYLOWSSLSKASDTAMTYCARHVDVGATIGGYYHYHGMVDWG 135
 QY 121 QGTTVTSS 129

DB 136 QGTTVTSS 144
 |||||
 RESULT 11
 ID AEA18549 standard; protein; 474 AA.
 XX
 AC AEA18549;
 XX
 DT 28-JUL-2005 (first entry)
 DE Variant of the heavy chain of anti-CD40 antibody CHIR-5.9.
 KW cytostatic; gene therapy; neoplasm; solid tumor; CD40; heavy chain;
 KW antibody CHIR-5.9; antibody therapy; ss.
 XX
 OS Synthetic.
 PN WO2005044305-A2.
 XX
 PD 19-MAY-2005.
 XX
 PF 04-NOV-2004; 2004WO-US036955.
 XX
 PR 04-NOV-2003; 2003US-0517337P.
 PR 26-NOV-2003; 2003US-0525579P.
 PR 27-APR-2004; 2004US-0565634P.
 PR 27-APR-2004; 2004US-0565710P.
 XX
 PA (CHIR) CHIRON CORP.
 PI Long L, Luqman M, Yabannavar A, Zaror I;
 XX
 DR WPI; 2005-346956/35.
 XX
 XX Treating human subjects for solid tumors that express CD40 cell-surface antigen comprises administering to the subject an amount of a human antagonist anti-CD40 monoclonal antibody that specifically binds to the CD40 antigen.
 XX
 PS Claim 1; SEQ ID NO 8; 123pp; English.
 XX
 CC The specification describes a method of treating a human subject for a solid tumor comprising carcinoma cells expressing CD40 antigen. The method comprises administering to the subject an amount of a human anti-CD40 monoclonal antibody that is capable of specifically binding to the CD40 antigen, the monoclonal antibody being free of significant agonist activity when bound to CD40 antigen. The method of the invention is useful for treating solid tumors expressing the CD40 cell-surface antigen, such as sarcomas or carcinoma of the lungs, breasts, ovary, skin, colon or urinary bladder, or in manufacturing medicaments for the treatment of such diseases. The present sequence represents a variant of the heavy chain of anti-CD40 monoclonal antibody CHIR-5.9, comprising a Ser for Ala substitution at site 158. This antibody represents an antibody which can be used in the method of the invention.
 XX
 SQ Sequence 474 AA;
 Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVWRMPGKGLWGMGIYPGSDSTRY 60
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVWRMPGKGLWGMGIYPGSDSTRY 79
 QY 61 SPSPGQQTATISADKSIATYLOWSSLSKASDTAMTYCARHVDVGATIGGYYHYHGMVDWG 120
 DB 80 SPSPGQQTATISADKSIATYLOWSSLSKASDTAMTYCARHVDVGATIGGYYHYHGMVDWG 135
 QY 121 QGTTVTSS 129

Db 136 QGTTVTVSS 144

RESULT 12
AEAL0642
ID AEA10642 standard; protein; 474 AA.
XX
AC AEA10642;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human anti-CD40 monoclonal antibody 5.9 heavy chain variant protein.
XX
KW multiple myeloma; hematological disease; immune disorder;
KW antibody therapy; cytostatic; gene therapy; CD40; monoclonal antibody;
KW heavy chain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..19
FT /note= "Leader region"
FT Region 20..144
FT /note= "Variable region"
FT Region 145..474
FT /note= "Constant region"
FT Misc-difference 158
FT /note= "Wild-type Ala has been substituted by Ser"
XX
PN WO2005044855-A2.
XX
XX 19-MAY-2005.
XX
XX 04-NOV-2004; 2004WO-US037281.
XX
XX 04-NOV-2003; 2003US-0517337P.
XX 26-NOV-2003; 2003US-0525579P.
XX 26-APR-2004; 2004US-0565709P.
XX 27-APR-2004; 2004US-0565710P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Long L, Luqman M, Yabannavar A, Zaror I;
XX WPI; 2005-347055/35.
XX
XX Treating human subjects for multiple myeloma comprises administering to
XX the subject an amount of a human antagonist anti-CD40 monoclonal antibody
XX that specifically binds to the CD40 antigen.
XX
XX Claim 1; SEQ ID NO 8; 115pp; English.
XX
XX The invention relates to a novel method for treating a human subject for
XX multiple myeloma comprising administering to the subject an amount of a
XX human anti-CD40 monoclonal antibody that specifically binds to a human
XX CD40 antigen expressed on the surface of a human CD40-expressing cell and
XX that is free of significant agonist activity, where the binding of the
XX antibody to the CD40 antigen expressed on the surface of the cell results
XX in inhibition of the growth or differentiation of the cell. Multiple
XX myeloma is a B-cell malignancy characterized by latent accumulation of
XX secretory plasma cells in the bone marrow, these cells having a low
XX proliferative index and an extended life span. The disease ultimately
XX attacks bones and bone marrow, resulting in multiple tumors and regions
XX throughout the skeletal system. The method of the invention demonstrates
XX cytostatic and gene therapy applications and may be useful for treating
XX multiple myeloma or in manufacturing medicaments for the treatment of
XX such a disease. The current sequence is that of the human anti-CD40
XX monoclonal antibody 5.9 heavy chain variant protein of the invention.
SQ Sequence 474 AA;

Query Match 89.1%; Score 623; DB 9; Length 474;
Best Local Similarity 91.5%; Pred. No. 1.8e-48;

Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPKGLWMGIIYPGSDTRY 60
DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPKGLWMGIIYPGSDTRY 79
QY 61 SPSPGQATTSADKSIISTAYLQWSSLSKASDTAMTYCARHVDVGATIGYGYHHGMDVWG 120
DB 80 SPSPGQATTSADKSIISTAYLQWSSLSKASDTAMTYCARHVDVGATIGYGYHHGMDVWG 135
QY 121 QGTTVTVSS 129
DB 136 QGTTVTVSS 144

RESULT 13
AEAL0641
ID AEA10641 standard; protein; 474 AA.
XX
AC AEA10641;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human anti-CD40 monoclonal antibody 5.9 heavy chain protein.
XX
KW multiple myeloma; hematological disease; immune disorder;
KW antibody therapy; cytostatic; gene therapy; CD40; monoclonal antibody;
KW heavy chain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..19
FT /note= "Leader region"
FT Region 20..144
FT /note= "Variable region"
FT Region 145..474
FT /note= "Constant region"
FT Misc-difference 158
FT /note= "A variant exists in which wild-type Ala may be
FT substituted by Ser"
XX
XX WO2005044855-A2.
XX
XX 19-MAY-2005.
XX
XX 04-NOV-2004; 2004WO-US037281.
XX
XX 04-NOV-2003; 2003US-0517337P.
XX 26-NOV-2003; 2003US-0525579P.
XX 26-APR-2004; 2004US-0565709P.
XX 27-APR-2004; 2004US-0565710P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Long L, Luqman M, Yabannavar A, Zaror I;
XX WPI; 2005-347055/35.
XX
XX Treating human subjects for multiple myeloma comprises administering to
XX the subject an amount of a human antagonist anti-CD40 monoclonal antibody
XX that specifically binds to the CD40 antigen.
XX
XX Claim 1; SEQ ID NO 7; 115pp; English.
XX
XX The invention relates to a novel method for treating a human subject for
XX multiple myeloma comprising administering to the subject an amount of a
XX human anti-CD40 monoclonal antibody that specifically binds to a human
XX CD40 antigen expressed on the surface of a human CD40-expressing cell and
XX that is free of significant agonist activity, where the binding of the
XX antibody to the CD40 antigen expressed on the surface of the cell results
XX in inhibition of the growth or differentiation of the cell. Multiple
XX myeloma is a B-cell malignancy characterized by latent accumulation of
XX secretory plasma cells in the bone marrow, these cells having a low
XX proliferative index and an extended life span. The disease ultimately
XX attacks bones and bone marrow, resulting in multiple tumors and regions
XX throughout the skeletal system. The method of the invention demonstrates
XX cytostatic and gene therapy applications and may be useful for treating
XX multiple myeloma or in manufacturing medicaments for the treatment of
XX such a disease. The current sequence is that of the human anti-CD40
XX monoclonal antibody 5.9 heavy chain variant protein of the invention.
SQ Sequence 474 AA;

CC secretory plasma cells in the bone marrow, these cells having a low
 CC proliferative index and an extended life span. The disease ultimately
 CC attacks bones and bone marrow, resulting in multiple tumors and regions
 CC throughout the skeletal system. The method of the invention demonstrates
 CC cytostatic and gene therapy applications and may be useful for treating
 CC multiple myeloma or in manufacturing medicaments for the treatment of
 CC such a disease. The current sequence is that of the human anti-CD40
 CC monoclonal antibody 5.9 heavy chain protein of the invention.
 XX
 XX Sequence 474 AA;

Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
 QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWRQMPGKGLWGMIIYPGSDTRY 60
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWRQMPGKGLWGMIIYPGSDTRY 79
 QY 61 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120
 DB 80 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 135
 QY 121 QGTTVTSS 129
 DB 136 QGTTVTSS 144

RESULT 14
 AED25714
 ID AED25714 standard; protein; 474 AA.
 AC AED25714;
 DT 01-DEC-2005 (first entry)
 DE Monoclonal anti-CD40-antibody CHIR-5.9 heavy chain.
 KW cytostatic; monoclonal antibody; antibody therapy; cancer; neoplasm;
 KW CHIR-5.9; heavy chain.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 20..474
 FT /note= "Mature monoclonal anti-CD40-antibody CHIR-5.9
 FT heavy chain"
 FT Region 20..144
 FT /note= "Monoclonal anti-CD40-antibody CHIR-5.9 heavy
 FT chain variable region"
 FT Region 145..474
 FT /note= "Monoclonal anti-CD40-antibody CHIR-5.9 heavy
 FT chain constant region"
 XX
 XX WO200504294-A2.
 XX
 XX 19-MAY-2005.
 XX
 XX 04-NOV-2004; 2004WO-US036958.
 XX
 XX 04-NOV-2003; 2003US-0517337P.
 XX 26-NOV-2003; 2003US-0525579P.
 XX 27-APR-2004; 2004US-0565710P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Long L, Luqman M, Yabannavar A, Zaror I, Hurst D;
 XX Lopes De Menezes DE;
 XX WPI; 2005-746884/76.
 XX

Treating human subject for cancer comprising neoplastic cells expressing
 CD40 antigen, by administering combination therapy including
 administration of anti-CD40 antibody e.g. CHIR-5.9, in combination with
 interleukin-2, to subject.

Claim 1; SEQ ID NO 7; 204pp; English.

The invention describes a method of treating (M1) a human subject for
 cancer comprising neoplastic cells expressing CD40 antigen. The method
 involves administering to the subject, a combination therapy including
 administration of an anti-CD40 antibody in combination with an
 interleukin-2 (IL-2), where the anti-CD40 antibody is the monoclonal
 antibody CHIR-5.9 or CHIR-12.12. (M1) is useful for treating a human
 subject for cancer comprising neoplastic cells expressing CD40 antigen,
 where the cancer is a B cell-related cancer or solid tumor. The B cell-
 related cancer is chosen from non-Hodgkin's lymphoma, chronic lymphocytic
 leukemia, multiple myeloma, B cell lymphoma, high-grade B cell lymphoma,
 intermediate-grade B cell lymphoma, low-grade B cell lymphoma, B cell
 acute lymphoblastic leukemia, myeloblastic leukemia, Hodgkin's disease,
 plasmacytoma, follicular lymphoma, follicular mixed small cleaved lymphoma,
 follicular large cell lymphoma, follicular mixed small cleaved lymphoma,
 diffuse small cleaved cell lymphoma, diffuse mixed small lymphocytic lymphoma,
 diffuse small cleaved cell lymphoma, diffuse small lymphocytic lymphoma,
 prolymphocytic leukemia, lymphoplasmacytic lymphoma, marginal zone
 lymphoma, mucosal associated lymphoid tissue lymphoma, monocytoid B cell
 lymphoma, splenic lymphoma, hairy cell leukemia, diffuse large cell
 lymphoma, mediastinal large B cell lymphoma, lymphomatoid granulomatosis,
 intravascular lymphomatosis, diffuse mixed cell lymphoma, diffuse large
 cell lymphoma, immunoblastic lymphoma, Burkitt's lymphoma, AIDS-related
 lymphoma and mantle cell lymphoma. The solid tumor is chosen from urinary
 bladder carcinoma, breast carcinoma, liver carcinoma, gastric carcinoma,
 colon carcinoma, prostate cancer, renal cell carcinoma, nasopharyngeal
 carcinoma, squamous cell carcinoma, thyroid papillary carcinoma,
 melanoma, ovarian carcinoma, lung carcinoma, cervical carcinoma and
 sarcomas. This is the amino acid sequence of human monoclonal anti-CD40-
 antibody CHIR-5.9 heavy chain.

Sequence 474 AA;

Query Match 89.1%; Score 623; DB 9; Length 474;
 Best Local Similarity 91.5%; Pred. No. 1.8e-48;
 Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWRQMPGKGLWGMIIYPGSDTRY 60
 DB 20 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGVWRQMPGKGLWGMIIYPGSDTRY 79
 QY 61 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 120
 DB 80 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVWG 135
 QY 121 QGTTVTSS 129
 DB 136 QGTTVTSS 144

RESULT 15
 AED25715
 ID AED25715 standard; protein; 474 AA.
 AC AED25715;
 DT 01-DEC-2005 (first entry)
 DE Monoclonal anti-CD40-antibody CHIR-5.9 heavy chain A1585.
 KW cytostatic; monoclonal antibody; antibody therapy; cancer; neoplasm;
 KW CHIR-5.9; heavy chain; mutein.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 158
 FT /note= "Wild type Ala substituted by Ser"

Search completed: April 25, 2007, 04:05:19
Job time : 111.873 secs

XX WO2005044294-A2.
XX 19-MAY-2005.
XX 04-NOV-2004; 2004WO-US036958.
XX 04-NOV-2003; 2003US-0517337P.
XX 26-NOV-2003; 2003US-0525579P.
XX 27-APR-2004; 2004US-0565710P.
XX (CHIR) CHIRON CORP.
XX Long L, Lugman M, Yabannavar A, Zaror I, Hurst D;
XX Lopes De Menezes DE;
XX WPI; 2005-746884/76.
XX
XX Treating human subject for cancer comprising neoplastic cells expressing
PT CD40 antigen, by administering combination therapy including
PT administration of anti-CD40 antibody e.g. CHIR-5.9, in combination with
PT interleukin-2, to subject.
XX
XX Claim 1; SEQ ID NO 8; 204pp; English.
XX
XX The invention describes a method of treating (M1) a human subject for
CC cancer comprising neoplastic cells expressing CD40 antigen. The method
CC involves administering to the subject, a combination therapy including
CC administration of an anti-CD40 antibody in combination with an
CC interleukin-2 (IL-2), where the anti-CD40 antibody is the monoclonal
CC antibody CHIR-5.9 or CHIR-12.12. (M1) is useful for treating a human
CC subject for cancer comprising neoplastic cells expressing CD40 antigen,
CC where the cancer is a B cell-related cancer or solid tumor. The B cell-
CC related cancer is chosen from non-Hodgkin's lymphoma, chronic lymphocytic
CC leukemia, multiple myeloma, B cell lymphoma, high-grade B cell lymphoma,
CC intermediate-grade B cell lymphoma, low-grade B cell lymphoma, B cell
CC acute lymphoblastic leukemia, myeloblastic leukemia, Hodgkin's disease,
CC plasmacytoma, follicular lymphoma, follicular small cleaved lymphoma,
CC follicular large cell lymphoma, follicular mixed small cleaved lymphoma,
CC diffuse small cleaved cell lymphoma, diffuse small lymphocytic lymphoma,
CC prolymphocytic leukemia, lymphoplasmacytic lymphoma, marginal zone
CC lymphoma, mucosal associated lymphoid tissue lymphoma, monocytoid B cell
CC lymphoma, splenic lymphoma, hairy cell leukemia, diffuse large cell
CC lymphoma, mediastinal large B cell lymphoma, lymphomatoid granulomatosis,
CC intravascular lymphomatosis, diffuse mixed cell lymphoma, diffuse large
CC cell lymphoma, immunoblastic lymphoma, Burkitt's lymphoma, AIDS-related
CC lymphoma and mantle cell lymphoma. The solid tumor is chosen from urinary
CC bladder carcinoma, breast carcinoma, liver carcinoma, gastric carcinoma,
CC colon carcinoma, prostate cancer, renal cell carcinoma, nasopharyngeal
CC carcinoma, squamous cell carcinoma, thyroid papillary carcinoma,
CC melanoma, ovarian carcinoma, lung carcinoma, cervical carcinoma and
CC sarcomas. This is the amino acid sequence of human monoclonal anti-CD40-
CC antibody CHIR-5.9 heavy chain A158S.
XX
XX Sequence 474 AA;
XX
XX Query Match 89.1%; Score 623; DB 9; Length 474;
XX Best Local Similarity 91.5%; Pred. No. 1.8e-48;
XX Matches 118; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
XX
XX 1 EVQLVDSGAEVKKPGSKLKSCGSGYSTFTSYWIGVWRQMPGKLEWGMGIYPGDSDTRY 60
XX |||||
XX 20 EVQLVDSGAEVKKPGSKLKSCGSGYSTFTSYWIGVWRQMPGKLEWGMGIYPGDSDTRY 79
XX |||||
XX 61 SPSPFQQTATISADKSIATYLOWSSLKASDTAMCYCARHVDVGATIGGVYVYHGMVWG 120
XX |||||
XX 80 SPSPFQQTATISADKSIATYLOWSSLKASDTAMCYCAR----GTAGRDYVYVYHGMVWG 135
XX |||||
XX 121 QGTTVTVSS 129
XX |||||
XX 136 QGTTVTVSS 144

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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 10 Seconds
(without alignments)
1261.509 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVQLVQSGAEVKKPGESLK.....YYHHGMDVWGQGTITVTVSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609.5	87.2	136	2 A49047	Ig heavy chain V r
2	587.5	84.0	134	2 PH1422	Ig heavy chain V r
3	576.5	82.5	139	2 PH1558	Ig heavy chain V r
4	574	82.1	123	2 C36006	Ig heavy chain V r
5	564	80.7	113	2 PH1428	Ig heavy chain V r
6	561	80.3	123	2 S38492	Ig heavy chain - h
7	561	80.3	144	2 PH1563	Ig heavy chain V r
8	558	79.8	127	2 PH1414	Ig heavy chain V r
9	553.5	79.2	141	2 S31685	Ig heavy chain V r
10	552.5	79.0	147	2 PH1561	Ig heavy chain V r
11	547	78.3	123	2 PH1423	Ig heavy chain V r
12	546	78.1	127	2 PH1415	Ig heavy chain V r
13	546	78.1	136	2 PH1559	Ig heavy chain V r
14	545	78.0	127	2 PH1420	Ig heavy chain V r
15	542.5	77.6	126	2 PH1419	Ig heavy chain V r
16	539	77.1	138	2 PH1565	Ig heavy chain V r
17	536.5	76.8	126	2 PH1417	Ig heavy chain V r
18	536.5	76.8	126	2 PH1418	Ig heavy chain V r
19	529.5	75.8	126	2 PH1416	Ig heavy chain V r
20	529	75.7	117	2 S19670	Ig heavy chain V r
21	528	75.5	123	2 PH1413	Ig heavy chain V r
22	527.5	75.5	126	2 PH1424	Ig heavy chain V r
23	527	75.4	128	2 S16685	Ig heavy chain V r
24	523	74.8	138	2 PH1564	Ig heavy chain V r
25	521	74.5	127	2 PH1411	Ig heavy chain V r
26	519	74.2	98	2 S26907	Ig heavy chain V r
27	519	74.2	101	2 S12424	Ig heavy chain V r
28	519	74.2	102	2 PH1279	Ig heavy chain V r
29	519	74.2	115	2 PH1557	Ig heavy chain V r

30	517	74.0	119	2 S36257	Ig heavy chain V r
31	516	73.8	102	2 PH1266	Ig heavy chain V r
32	516	73.8	102	2 PH1252	Ig heavy chain V r
33	515	73.7	117	2 S19669	Ig heavy chain V r
34	514	73.5	101	2 S12428	Ig heavy chain V r
35	514	73.5	117	2 A28846	Ig heavy chain pre
36	513	73.4	102	2 PH1281	Ig heavy chain V r
37	513	73.4	102	2 PH1271	Ig heavy chain V r
38	513	73.4	102	2 PH1278	Ig heavy chain V r
39	512	73.2	109	2 PH1672	Ig heavy chain V r
40	511	73.1	102	2 PH1254	Ig heavy chain V r
41	510.5	73.0	122	2 FC4280	anti-SS-A/Ro 60K p
42	510	73.0	102	2 PH1258	Ig heavy chain V r
43	510	73.0	144	2 E41287	Ig heavy chain pre
44	508.5	72.7	137	2 PH1562	Ig heavy chain V r
45	507.5	72.6	122	2 PH1426	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A49047

Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (fr
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C;Accession: A49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: A49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-136 <VIC>
A;Cross-references: UNIPARC:UPI0000176C6A
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113206, NCBIP:113207)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match	87.2%;	Score 609.5;	DB 2;	Length 136;
Best Local Similarity	87.4%;	Pred. No. 6.9e-48;		
Matches 118;	Conservative 4;	Mismatches 4;	Indels 9;	Gaps 3;
Qy	1	EVQLVQSGAEVKKPGESLKISKSGSYFTSYIGWVROMPGKLEWNGIIPGDS	TRY 60	
Db	5	EVQLVQSGAEVKKPGESLKISKSGSYFTSYIGWVROMPGKLEWNGIIPGDS	TRY 64	
Qy	61	SPSFQQAATISADKSI STAYLQWSSLKASDTAMYCAR---	HVDVGTATGGY--YYH 114	
Db	65	SPSFQQAATISADKSI STAYLQWSSLKASDTAMYCARQSYGYDFRS---	GYTPAYYYY 121	
Qy	115	GMDVWGQGTITVTVSS	129	
Db	122	GMDVWGQGTITVTVSS	136	

RESULT 2

PH1422

Ig heavy chain V region (clone P3-69) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1422
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin B response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1422
A;Molecule type: mRNA
A;Residues: 1-134 <VAN>
A;Cross-references: UNIPARC:UPI0000176A2E

A:Experimental source: PBMC
A:Note: the authors translated the codon ATG for residue 93 as Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 587.5; DB 2; Length 134;
Best Local Similarity 85.6%; Pred. No. 6.4e-46;
Matches 113; Conservative 3; Mismatches 11; Indels 5; Gaps 2;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 60

DB 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIAVRQMPKGLEWNGIIPGSDTRY 60

QY 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARH---VDVGATIGGYYYHGM 117

DB 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARHMEYVYSGSSDYIIY---MD 118

QY 118 VMGQGTITVSS 129

DB 119 VMGKGTITVSS 130

RESULT 3

PH1558

Ig heavy chain V region (clone DOB) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996

C:Accession: PH1558

R:Rassenti, L.Z.; Kipps, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A:Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymph

A:Reference number: PH1557; MUID:93210459; PMID:7681468

A:Accession: PH1558

A:Molecule type: DNA

A:Residues: 1-139 <RAS>

A:Cross-references: UNIPARC:UPI0000176B81

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-115/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 576.5; DB 2; Length 139;
Best Local Similarity 85.3%; Pred. No. 6.5e-45;
Matches 110; Conservative 1; Mismatches 11; Indels 7; Gaps 1;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 60

DB 18 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 77

QY 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHGM 120

DB 78 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARSISSG-----YYSNFDYWG 130

QY 121 QGTITVSS 129

DB 131 QGTLTVSS 139

RESULT 4

C36006

Ig heavy chain V region (83p2) - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C:Accession: C36006

R:Schoeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A:Reference number: A36005; MUID:90349571; PMID:21117273

A:Accession: C36006

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 <SCH>

A:Cross-references: UNIPARC:UPI0000176C49; GB:M34022

C:Genetics:

A:Gene: GDB:IGH0; IGHY1

A:Cross-references: GDB:118731; OMIM:146910

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 574; DB 2; Length 123;
Best Local Similarity 85.3%; Pred. No. 9.6e-45;
Matches 110; Conservative 5; Mismatches 8; Indels 6; Gaps 2;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 60

DB 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 60

QY 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHGM 120

DB 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARH---NSQTGSLWYF---DLWG 114

QY 121 QGTITVSS 129

DB 115 QGTLTVSS 123

RESULT 5

PH1428

Ig heavy chain V region (clone VH5-1R1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 28-May-1999

C:Accession: PH1428

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of st

dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1428

A:Molecule type: mRNA

A:Residues: 1-113 <VAN>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 564; DB 2; Length 113;
Best Local Similarity 84.5%; Pred. No. 7e-44;
Matches 109; Conservative 0; Mismatches 4; Indels 16; Gaps 1;

QY 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 60

DB 1 EVQLVQSGAEVKKPESLKISKCKSGYSFTSYWIGVROMPKGLEWNGIIPGSDTRY 60

QY 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCARHVDVGATIGGYYYHGM 120

DB 61 SPSPGQQTISADKSIKSTAYLQWSSLKASDTAMYCAR-----AFDVGW 104

QY 121 QGTITVSS 129

DB 105 QGTMVTSS 113

RESULT 6

S38492

Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38492

R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.

submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from a pl

A:Reference number: S38488

A:Accession: S38492

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-123 <VAR>

A;Cross-references: UNIPARC:UPI000011654D; EMBL:Z23034; NID:9414031; PIDN:CAA80569.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 561; DB 2; Length 123;
Best Local Similarity 83.2%; Pred. No. 1.4e-43;
Matches 109; Conservative 3; Mismatches 9; Indels 10; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

Db 1 QVQLVSGAEVKKPGESLKISCKSGYSFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGYYHYHG--MDV 118

Db 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYICARR-----RYSYAQHDWYFDL 112

QY 119 WGQTTVTVSS 129

Db 113 WGRGLTVTVSS 123

RESULT 7

PH1563

IG heavy chain V region (clone PET) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PH1563
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphoma
A;Reference number: PH1557; MUID:93210459; PMID:7681468
A;Accession: PH1563

A:Molecule type: DNA

A:Residues: 1-144 <RAS>

A;Cross-references: UNIPARC:UPI0000176963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 561; DB 2; Length 144;
Best Local Similarity 84.5%; Pred. No. 1.7e-43;
Matches 109; Conservative 3; Mismatches 15; Indels 2; Gaps 1;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

Db 18 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWISWVROMPGKLEWNGRIDPSDYTNV 77

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGYYHYHGMDVWG 120

Db 78 SPSPFOGHTVISADKSIISTAYLQWSSLSKASDTAMYICARLLYGAAAWGYYTNY--MDVWG 135

QY 121 QGTTVTVSS 129

Db 136 KGIITVTVSS 144

RESULT 8

PH1414

IG heavy chain V region (clone P1-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1414
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of somatic mutations.

A;Reference number: PH1409; MUID:93115676; PMID:8418213

A;Accession: PH1414

A:Molecule type: mRNA

A:Residues: 1-127 <VAN>

A;Cross-references: UNIPARC:UPI000017694E

A;Experimental source: PBMC

A;Note: the authors translated the codon TTG for residue 119 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 558; DB 2; Length 127;
Best Local Similarity 84.5%; Pred. No. 2.7e-43;
Matches 109; Conservative 3; Mismatches 11; Indels 6; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

Db 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGYYHYHGMDVWG 120

Db 61 SPSPFOQATISADKSIISTAYLQWSSLSKATDTAMYICARR-DYGD-----YQSTGGFDPWG 114

QY 121 QGTTVTVSS 129

Db 115 QGTLTVTVSS 123

RESULT 9

S31685

IG heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S31685
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31685
A;Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-141 <CUI>

A;Cross-references: UNIPARC:UPI0000116462; EMBL:Z14183; NID:931033; PIDN:CAA78552.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 553.5; DB 2; Length 141;
Best Local Similarity 82.3%; Pred. No. 7.7e-43;
Matches 107; Conservative 3; Mismatches 12; Indels 7; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKSGYSFTSYWIGVROMPGKLEWNGIIPGDSSTRY 60

Db 20 EVOLVSGAEVKKPGESLRISCKSGYSFTSYWISWVROMPGKLEWNGRIDPSDYTNV 79

QY 61 SPSPFOQATISADKSIISTAYLQWSSLSKASDTAMYICARHVDVGATIGGYYHYHGMDVWG 120

Db 80 SPSPFOGHTVISADKSIISTAYLQWSSLSKASDTAMYICARR-----GVRYGYYTNY--MDVWG 132

QY 121 QGTTVTVSS 129

Db 133 KGIITVTVSS 141

RESULT 10

PH1561

IG heavy chain V region (clone CAV) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PH1561
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphoma

A;Reference number: PH1557; MUID:93210459; PMID:7681468

A;Accession: PH1561

A:Molecule type: DNA

A:Residues: 1-147 <RAS>

A;Cross-references: UNIPARC:UPI0000176961
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 552.5; DB 2; Length 147;
Best Local Similarity 83.2%; Pred. No. 9.9e-43;
Matches 109; Conservative 4; Mismatches 15; Indels 3; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGIIPGDSSTRY 60
DB 18 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGRIDPSYNYI 77
QY 61 SPSPFOQATISADKSIKTAYLQWSSLKASDTAMYICARHVDVCGATIG--GYTYYHGMVDV 118
DB 78 SPSPFOGHVTTISADKSIKTAYLQWSSLKASDTAMYICARQIAGIAAGMGWGPYYIY--MDV 136
QY 119 WGQGTVTIVSS 129
DB 137 WGKGTTVTIVSS 147

RESULT 11
PHI423
Ig heavy chain V region (clone P3-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PHI423
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
A;Reference number: PHI409; MUID: 93115676; PMID: 8418213
A;Accession: PHI423
A;Molecule type: mRNA
A;Residues: 1-123 <VAN>
A;Cross-references: UNIPARC:UPI0000176958
A;Experimental source: PMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 547; DB 2; Length 123;
Best Local Similarity 80.6%; Pred. No. 2.6e-42;
Matches 104; Conservative 4; Mismatches 11; Indels 10; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGIIPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIAVVRQMPGKLEWNGIIPGDSSTRY 60
QY 61 SPSPFOQATISADKSIKTAYLQWSSLKASDTAMYICARHVDVCGATIGGYTYYHGMVDVWG 120
DB 61 SPSPFOQVTTISADKSIKTAYLQWSSLKASDTAIYICARHAD-----NFDWFQIWNG 110
QY 121 QGTIVTVSS 129
DB 111 QGTLVTVSS 119

RESULT 12
PHI415
Ig heavy chain V region (clone P1-57) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PHI415
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
A;Reference number: PHI409; MUID: 93115676; PMID: 8418213
A;Accession: PHI415
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>

A;Cross-references: UNIPARC:UPI000017694F
A;Experimental source: PMC
A;Note: the authors translated the codon TTG for residue 118 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 546; DB 2; Length 127;
Best Local Similarity 83.7%; Pred. No. 3.3e-42;
Matches 108; Conservative 2; Mismatches 13; Indels 6; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGIIPGDSSTRY 60
DB 1 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGIIPGDSSTRY 60
QY 61 SPSPFOQATISADKSIKTAYLQWSSLKASDTAMYICARHVDVCGATIGGYTYYHGMVDVWG 120
DB 61 SPSPFOQVTTISADKSIKTAYLQWSSLKASDTAMYICARR-DYGD-----YQSTGTFDPWG 114
QY 121 QGTIVTVSS 129
DB 115 QGTLVTVSS 123

RESULT 13
PHI559
Ig heavy chain V region (clone HAN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PHI559
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia.
A;Reference number: PHI557; MUID: 93210459; PMID: 7681468
A;Accession: PHI559
A;Molecule type: DNA
A;Residues: 1-136 <RAS>
A;Cross-references: UNIPARC:UPI000176A21
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 546; DB 2; Length 136;
Best Local Similarity 82.2%; Pred. No. 3.5e-42;
Matches 106; Conservative 2; Mismatches 11; Indels 10; Gaps 1;

QY 1 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGIIPGDSSTRY 60
DB 18 EVQLVQSGAEVKKPGESLKISKCKSGSYFTSYWIGVVRQMPGKLEWNGIIPGDSSTRY 77
QY 61 SPSPFOQATISADKSIKTAYLQWSSLKASDTAMYICARHVDVCGATIGGYTYYHGMVDVWG 120
DB 78 SPSPFOQVTTISADKSIKTAYLQWSSLKASDTAMYICAR-----LYGDFSTVDVWG 127
QY 121 QGTIVTVSS 129
DB 128 QGTLVTVSS 136

RESULT 14
PHI420
Ig heavy chain V region (clone P2-55) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PHI420
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.
A;Reference number: PHI409; MUID: 93115676; PMID: 8418213
A;Accession: PHI420
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>

A;Cross-references: UNIPARC:UPI0000176B9A

A;Experimental source: PHMC

A;Note: the authors translated the codon CTT for residue 101 as Phe

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 545; DB 2; Length 127;
Best Local Similarity 79.8%; Pred. No. 4e-42;
Matches 103; Conservative 8; Mismatches 12; Indels 6; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDDTRY 60

Db 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDDTRY 60

QY 61 SPSFQOQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYYYHGMVDVWG 120

Db 61 SPSFQOQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYYYHGMVDVWG 120

QY 121 QGTTVTVSS 129

Db 115 RGTLTVPVS 123

RESULT 15

PHI419

IG heavy chain V region (clone P2-54) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C;Accession: PHI419

R;Van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.

A;Reference number: PHI409; MUID:93115676; PMID:8418213

A;Accession: PHI419

A;Molecule type: mRNA

A;Residues: 1-126 <VAN>

A;Cross-references: UNIPARC:UPI0000176953

A;Experimental source: PHMC

A;Note: the authors translated the codon ACT for residue 107 as Ser

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 542.5; DB 2; Length 126;
Best Local Similarity 79.1%; Pred. No. 6.7e-42;
Matches 102; Conservative 9; Mismatches 11; Indels 7; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDDTRY 60

Db 1 EVOLVQSGAEVKKPGESLKISCKSGSYSTSYWIGWVROMPGKLEWNGIIPGDSDDTRY 60

QY 61 SPSFQOQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYYYHGMVDVWG 120

Db 61 SPSFQOQATISADKSIATYLOWSSLKASDTAMYCARHVDVGATIGGYYYYHGMVDVWG 120

QY 121 QGTTVTVSS 129

Db 114 QGTMVTVSS 122

Search completed: April 25, 2007, 04:06:39
Job time : 9.83898 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 88 Seconds
(without alignments)
1574.822 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVQLVQSGAEVKKPGESLK.....YYHHGMDVMGQGTITVTS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt.8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441.5	63.2	475	Q5RE17_PONPY	Q5re17 pongo pygma
2	435.5	62.3	159	Q9GQSO_HUMAN	Q9Gqso homo sapien
3	418.5	59.9	118	Q9Z1C4_MOUSE	Q9Z1c4 mus musculus
4	407	58.2	479	Q3KQK2_MOUSE	Q3Kqk2 mus musculus
5	403	57.7	244	Q65ZC8_HUMAN	Q65zc8 homo sapien
6	398	56.9	483	Q52L51_MOUSE	Q52l51 mus musculus
7	395	56.5	614	Q7TWT6_MOUSE	Q7Twt6 mus musculus
8	394	56.4	458	Q5BJZ2_RAT	Q5Bjz2 rattus norv
9	392.5	56.2	617	Q4KML5_MOUSE	Q4Kml5 mus musculus
10	391.5	56.0	124	Q9UL92_HUMAN	Q9Ul92 homo sapien
11	391.5	56.0	613	Q8VCX7_MOUSE	Q8vcx7 mus musculus
12	390.5	55.9	500	Q9BRV0_HUMAN	Q9Brv0 homo sapien
13	389.5	55.7	143	Q924P9_MOUSE	Q924p9 mus musculus
14	388	55.4	468	Q559W9_MOUSE	Q559w9 mus musculus
15	387	55.4	121	HV01_MOUSE	P01745 mus musculus
16	386.5	55.3	143	Q91V67_MOUSE	Q91v67 mus musculus
17	385.5	55.2	498	Q6N041_HUMAN	Q6n041 homo sapien
18	384.5	55.0	145	Q924Q6_MOUSE	Q924q6 mus musculus
19	384	54.9	119	Q9UL94_HUMAN	Q9Ul94 homo sapien
20	383	54.8	168	Q8VDC3_MOUSE	Q8vdc3 mus musculus
21	382.5	54.7	143	Q924Q5_MOUSE	Q924q5 mus musculus
22	382.5	54.7	482	Q2T9K9_MOUSE	Q2t9k9 mus musculus
23	382.5	54.7	590	Q4V9V8_MOUSE	Q4v9v8 mus musculus
24	382	54.6	125	Q9UL95_HUMAN	Q9Ul95 homo sapien
25	382	54.6	146	Q924Q3_MOUSE	Q924q3 mus musculus
26	382	54.6	474	Q8R3H6_MOUSE	Q8r3h6 mus musculus
27	382	54.6	481	Q91WT1_MOUSE	Q91wt1 mus musculus
28	381.5	54.5	145	Q924R4_MOUSE	Q924r4 mus musculus
29	381	54.5	142	Q924Q2_MOUSE	Q924q2 mus musculus
30	381	54.5	144	Q924P5_MOUSE	Q924p5 mus musculus
31	381	54.5	470	Q7TMK1_MOUSE	Q7tmk1 mus musculus

Query Match

Best Local Similarity 63.2%; Score 441.5; DB 2; Length 475;

Matches 86; Conservative 16; Mismatches 23; Indels 3; Gaps 2;

32	380.5	54.4	145	2	Q924R3_MOUSE	Q924r3 mus musculus
33	380.5	54.4	484	2	Q3SYJ4_MOUSE	Q3syj4 mus musculus
34	379	54.2	146	2	Q924R8_MOUSE	Q924r8 mus musculus
35	378.5	54.1	143	2	Q924Q0_MOUSE	Q924q0 mus musculus
36	378.5	54.1	145	2	Q924Q9_MOUSE	Q924q9 mus musculus
37	378.5	54.1	482	2	Q8K172_MOUSE	Q8k172 mus musculus
38	378	54.1	119	2	Q9GYZ2_MOUSE	Q9gyz2 mus musculus
39	378	54.1	120	1	HV03_MOUSE	P01747 mus musculus
40	377.5	54.0	145	2	Q924R1_MOUSE	Q924r1 mus musculus
41	377	53.9	147	2	Q925S3_MOUSE	Q925s3 mus musculus
42	377	53.9	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
43	377	53.9	598	2	Q568Y0_RAT	Q568y0 rattus norv
44	376.5	53.9	139	1	HV07_MOUSE	P01751 mus musculus
45	376.5	53.9	143	2	Q924R7_MOUSE	Q924r7 mus musculus

ALIGNMENTS

RESULT 1
Q5RE17_PONPY
ID Q5RE17_PONPY PRELIMINARY; PRT; 475 AA.
AC Q5RE17;
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 27-JUN-2006, entry version 19.
DE Hypothetical protein DKFp469C2335.
GN Name=DKFp469C2335;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Pouscka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
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CC
CC EMBL; CR857722; CAH89990.1; -; mRNA.
DR SMR; Q5RE17; 21-475.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03597; IG_C1-set.
DR InterPro; IPRO03006; IG_MHC.
DR InterPro; IPRO03599; IG_sub.
DR InterPro; IPRO13106; IG_V-set.
DR InterPro; IPRO03596; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 475 AA; 51898 MW; 04BBD096A2CD529 CRC64;

QY 1 EVQLVQSGAEVKKPGESLKISKSGSYFTSYWIGVWVQMPGKGLWGMGIYPGSDTRY 60
 Db 20 DIQLVQSGAEVKKPGESLRISCKSGSYFTSYWIGVWVQMPGKGLWGMIDPNSGTRY 79
 QY 61 SPSPQGGATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVGVATIGGYYHYHGMVWG 120
 Db 80 NRSFEGHITISADMSISTAYLQWSSLKASDAIYYCAR-LRLSGT--NSYHKRSYFPQWG 136
 QY 121 QGTTTVSS 128
 Db 137 QGTLIVS 144
 RESULT 2
 Q96QSO HUMAN PRELIMINARY; PRT; 159 AA.
 AC Q96QSO;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 18-APR-2006, entry version 21.
 DE Putative matrix cell adhesion molecule-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tilson M.D.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AY039025; AAK82649.1; -; mRNA.
 DR HSP; P01869; 1A56.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 62.3%; Score 435.5; DB 2; Length 159;
 Best Local Similarity 60.6%; Pred. No. 1.7e-36;
 Matches 80; Conservative 22; Mismatches 25; Indels 5; Gaps 2;
 QY 1 EVQLVQSGAEVKKPGESLKISKSGSYFTSYWIGVWVQMPGKGLWGMGIYPGSDTRY 60
 Db 20 QVQLVQSGAEVKKPGASVKSCAKSGYFTSYWVWVQMPGKGLWGMVNPSCGARY 79
 QY 61 SPSPQGGATISADKSIISTAYLQWSSLKASDTAMYYCARHVDV---GATIGGYYHYHGM 117
 Db 80 SQKFGRLTMTDSTSYVMDLSRLSDTAVYFCAREMEITFGGAVSKGFIYY--GMD 137
 QY 118 VWGQTTTVSS 129
 Db 138 VWGQTTTVSS 149
 RESULT 3
 Q92IC4 MOUSE PRELIMINARY; PRT; 118 AA.
 ID Q92IC4;
 AC Q92IC4;
 DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1999, sequence version 1.
 DT 18-APR-2006, entry version 22.
 DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Balb/c;
 RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Mattis L.A., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT IgG2/G4 constant regions block human leukocyte binding to porcine
 RT endothelial cells.";
 RL Mol. Immunol. 34:441-452(1997).
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 CC -----
 DR EMBL; U78801; AAD00293.1; -; mRNA.
 DR HSP; P01751; 1NQ8.
 DR SMR; Q9ZIC4; 1-118.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin domain.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 13036 MW; 90EBC559D31EC4FC CRC64;
 Query Match 59.9%; Score 418.5; DB 2; Length 118;
 Best Local Similarity 58.9%; Pred. No. 6.6e-35;
 Matches 76; Conservative 23; Mismatches 19; Indels 11; Gaps 2;
 QY 1 EVQLVQSGAEVKKPGESLKISKSGSYFTSYWIGVWVQMPGKGLWGMGIYPGSDTRY 60
 Db 1 QVQVQSGAEALRPWASVKLSCKSGYFNFSYQWVQKQPGQGLEWIGAIYPGDGTSY 60
 QY 61 SPSPQGGATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVGVATIGGYYHYHGMVWG 120
 Db 61 TQKFRGKATLTADKSSSTAYMQLSLASEDSAVYYCARR-----TVGGYF-----DYWG 109
 QY 121 QGTTTVSS 129
 Db 110 QGTTTVSS 118
 RESULT 4
 Q3KQK2 MOUSE PRELIMINARY; PRT; 479 AA.
 ID Q3KQK2_MOUSE
 AC Q3KQK2;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 27-JUN-2006, entry version 8.
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
 RC old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smalhus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
 RC old;
 RG NIH MGC Project;
 RL Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 CC EMBL; BC106157; AAI06158.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1-set.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07654; C1-set; 2.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG-LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein; Immunoglobulin C region; Immunoglobulin domain;
 KW Membrane; Repeat; Transmembrane.
 SQ SEQUENCE 479 AA; 51745 MW; DB88E95F136BD78E CRC64;
 Query Match 58.2%; Score 407; DB 2; Length 479;
 Best Local Similarity 58.9%; Pred. No. 5.1e-33;
 Matches 76; Conservative 20; Mismatches 19; Indels 14; Gaps 2;
 QY 1 EVOLVSGAEVKKPGESLKISCKGSGYFTSYWIGVWRQMPGKLEWMIYPGSDTRY 60
 Db 20 QVQLQQSGAELASPASQSVKSPKSGYFTSYWIMQVWRQMPGKLEWMIYPGDGETRY 79
 QY 61 SPSFQQAATISADKSIATAYLQWSSLSKASDTAMYICARHVDVGATIGGYVYHGMVDVWG 120
 Db 80 SQKVGKATLTADKSSSTAYMQLSSLAEDSAVYICAR-----TFYF---DSWG 125
 QY 121 QGTTVTSS 129
 Db 126 QGTTLTSS 134
 RESULT 5
 Q65ZC8 HUMAN
 ID Q65ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
 AC Q65ZC8;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.

DT 18-APR-2006, entry version 10.
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97382799; PubMed=9219263; DOI=10.1038/nbt0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies";
 RL Nat. Biotechnol. 15:629-631(1997).
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 CC -----
 CC EMBL; Y13057; CAA73500.1; -; mRNA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR013106; Ig_V-set.
 DR InterPro; IPR003596; Ig_V-set_sub.
 DR Pfam; PF07686; V-set; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 FT NON_TER 1 1
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
 Query Match 57.7%; Score 403; DB 2; Length 244;
 Best Local Similarity 58.9%; Pred. No. 6e-33;
 Matches 76; Conservative 23; Mismatches 22; Indels 8; Gaps 2;
 QY 1 EVOLVSGAEVKKPGESLKISCKGSGYFTSYWIGVWRQMPGKLEWMIYPGSDTRY 60
 Db 1 QVQLVSGAEVKKPGESLKISCKGSGYFTSDHWHVWRQMPGKLEWMIYDPPNGDTRF 60
 QY 61 SPSFQQAATISADKSIATAYLQWSSLSKASDTAMYICARHVDVGATIGGYVYHGMVDVWG 120
 Db 61 AQRFQGRVTWTRDTSISAAVMEVSRSLRSDDTAVYICARE-GTGSAL-----YGMVDVWG 112
 QY 121 QGTTVTSS 129
 Db 113 QGTLVTSS 121
 RESULT 6
 Q52L51 MOUSE
 ID Q52L51 MOUSE PRELIMINARY; PRT; 483 AA.
 AC Q52L51;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 27-JUN-2006, entry version 16.
 DE LOC544903 protein.
 GN Name=LOC544903;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
 RC old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.A., Touchman J.W., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor; WAP-TGF alpha model. 7 months
RC old;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC094065; AAH94065.1; -; mRNA.
DR GO; GO:0016021; C:membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; P:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003599; IG_sub.
DR InterPro; IPR013106; IG_V-set.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 483 AA; 52167 MW; CQFDB9168795FEB4 CRC64;

Query Match 56.9%; Score 398; DB 2; Length 483;
Best Local Similarity 59.1%; Pred. No. 4.4e-32;
Matches 75; Conservative 20; Mismatches 22; Indels 10; Gaps 2;

QY 3 QLVSQAEVKKPGESLIKSGSYFTSYWIGWVRQMPKGLWGGIIPGDSITRYP 62
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
22 QLQSGAERVKGASVKISKASGVAFSGPWNWVKQRPKGLWIGRIYPGDGETHYSG 81
QY 63 SFQQTATISADKISTAYLQWSLKSADTAMYYCARHVDVGATIGYGYYYHYGMVWGQ 122
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 QPKGKATLTADKSSSTAYVQLNGLTSDSAVYFCAR-----GNWPYWY--LDVWGAG 131

QY 123 TTVTVSS 129
Db |||:|||||
132 TTVTVSS 138

RESULT 7
Q7TWT6_MOUSE PRELIMINARY; PRT; 614 AA.
AC Q7TWT6;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 25-JUL-2006, entry version 31.
DE MGC60843 protein.

```

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GN Name=Igh-6; Synonyms=MGC60843;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RC Pubmed=12477932; DOI=10.1073/pnas.242603899;
RG Mammalian Gene Collection Program Team;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.A., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC053409; AAH53409.1; -; mRNA.
DR HSSP; P01820; IGTJ.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IEA.
DR GO; GO:0003997; C:external side of plasma membrane; IEA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IEA.
DR GO; GO:0048471; C:perinuclear region; IEA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:000187; P:activation of MAPK activity; IEA.
DR GO; GO:0030333; P:antigen processing; IEA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IEA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IEA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IEA.
DR GO; GO:0038890; P:positive regulation of B cell proliferation; IEA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IEA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . . ; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003599; IG_sub.
DR InterPro; IPR013106; IG_V-set.
DR InterPro; IPR003596; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 4.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
KW Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.

```

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 CC EMBL; BC098504; AAH98504.1; -; mRNA.
 CC MGI; 96448; Igh-6.
 CC GO; GO:0013815; C:B cell receptor complex; IDA.
 CC GO; GO:0009897; C:external side of plasma membrane; IDA.
 CC GO; GO:0042571; C:immunoglobulin complex; circulating; IDA.
 CC GO; GO:0048471; C:perinuclear region; IDA.
 CC GO; GO:0003823; F:antigen binding; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0004888; F:transmembrane receptor activity; IDA.
 CC GO; GO:000187; P:activation of MAPK activity; IDA.
 CC GO; GO:0030333; P:antigen processing; IDA.
 CC GO; GO:003853; P:B cell receptor signaling pathway; IDA.
 CC GO; GO:0045022; P:early endosome to late endosome transport; IDA.
 CC GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
 CC GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
 CC GO; GO:0045807; P:positive regulation of endocytosis; IDA.
 CC GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. .; IDA.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_C1-set.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003599; Ig_sub.
 CC InterPro; IPR013106; Ig_V-set.
 CC Pfam; PF07654; C1-set; 4.
 CC Pfam; PF07686; V-set; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00407; IGc1; 2.
 CC PROSITE; PS00835; IG_LIKE; 5.
 CC PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin C region; Immunoglobulin domain; Membrane; Repeat;
 KW Transmembrane.
 SQ SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;

 Query Match 56.2%; Score 392.5; DB 2; Length 617;
 Best Local Similarity 55.8%; Pred. No. 2.1e-31;
 Matches 72; Conservative 23; Mismatches 27; Indels 7; Gaps 1;

 QY 1 EVOLVSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKLEWGMGIYPGDS DTRY 60
 DB 20 QVQLQSGAEAKPQASVKLSCKGSGYSTSYWIMHWKQRPQGQLEWIGVNPSSGYTKY 79
 QY 61 SPSPFQQAATISADKSIATYLOWSSLSKASDTAMYCARHVDVGVGATGGYVYHYHGMVNG 120
 DB 80 NQKFKDKATLTADKSSSTAYMQLSSLTYSVAVYICARR-----EGHLLWVYANDYWG 132
 QY 121 QGTTVTVSS 129
 DB 133 QGTSVTSS 141

 RESULT 10
 Q9UL92 HUMAN PRELIMINARY; PRT; 124 AA.
 AC Q9UL92;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License

 CC EMBL; AF035022; AAD56258.1; -; mRNA.
 CC HSSP; P01751; INQB.
 CC LinkHub; Q9UL92;
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig_sub.
 CC InterPro; IPR013106; Ig_V-set.
 CC InterPro; IPR003596; Ig_V-set_sub.
 CC Pfam; PF07686; V-set; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00406; IG; 1.
 CC PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin domain.
 FT NON_TER 1
 FT NON_TER 124 124
 SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

 Query Match 56.0%; Score 391.5; DB 2; Length 124;
 Best Local Similarity 58.0%; Pred. No. 4.2e-32;
 Matches 76; Conservative 19; Mismatches 27; Indels 9; Gaps 2;

 QY 1 EVOLVSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKLEWGMGIYPGDS DTRY 60
 DB 1 EVOLVESGAEVKKPGASVKSCASGYTSSYIMHWVRQAPGQGLEWGMGINPSGGSTSY 60
 QY 61 SPSPFQQAATISADKSIATYLOWSSLSKASDTAMYCARHVDVGVGATGGYVYHYHGMV 118
 DB 61 AQKFGQGVTRTSTSTVWELSSLSRSEDATVYICARGLYVVVPAFASRF-----DY 113
 QY 119 WGQGTITVTSS 129
 DB 114 WGQGTITVTSS 124

 RESULT 11
 Q8VCX7 MOUSE PRELIMINARY; PRT; 613 AA.
 ID Q8VCX7_MOUSE
 AC Q8VCX7;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 27-JUN-2006, entry version 33.
 DE Igh-6 protein.
 GN Name=Igh-6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Query Match	55.7%;	Score 389.5;	DB 2;	Length 143;
Best Local Similarity	56.6%;	Pred. No. 8e-32;		

Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
 QY 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60
 DB 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60
 QY 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
 DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
 QY 121 QGTLVTVSS 129
 DB 111 QGTLVTVSS 119

RESULT 2
 US-09-490-070A-26
 ; Sequence 26, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilag, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 ; White & McAuliffe
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,070A
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colin G. Sandercock, Esq.
 ; REGISTRATION NUMBER: 37629-0005
 ; REFERENCE/DOCKET NUMBER: 37629-0005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 912-2000
 ; TELEFAX: (202) 912-2020
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-070A-26

Query Match 82.7%; Score 578; DB 2; Length 119;
 Best Local Similarity 87.6%; Pred. No. 6.5e-48;
 Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
 QY 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60
 DB 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60
 QY 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
 DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120

Db 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 110
 QY 121 QGTLVTVSS 129
 DB 111 QGTLVTVSS 119
 RESULT 3
 US-09-490-153-26
 ; Sequence 26, Application US/09490153
 ; Patent No. 6706484
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilag, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,153
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025,769B
 ; FILING DATE: 18-FEB-1998
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 596-9000
 ; TELEFAX: (212) 596-9090
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-490-153-26

Query Match 82.7%; Score 578; DB 2; Length 119;
 Best Local Similarity 87.6%; Pred. No. 6.5e-48;
 Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
 QY 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60
 DB 1 EVQLVQSGAEVKPGESLKISCKSGSYFTSYWIGWRQMPGKGLWNGIILYPGDSSTRY 60
 QY 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
 DB 61 SPSPQGGATISADKSIISTAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGMVDWG 120
 QY 121 QGTLVTVSS 129
 DB 111 QGTLVTVSS 119

RESULT 4
US-09-490-324-26
; Sequence 26, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-490-324-26

Query Match 82.7%; Score 578; DB 2; Length 119;
Best Local Similarity 87.6%; Pred. No. 6.5e-48;
Matches 113; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
QY 1 EVLVQSGAEVKPGESLTKISCKGSGYSFTSYWIGWVRQMPGKLEWMIIPGDSSTRY 60
Db 1 EVLVQSGAEVKPGESLTKISCKGSGYSFTSYWIGWVRQMPGKLEWMIIPGDSSTRY 60
QY 61 SPSFGQATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGYVYHYHGMVWG 120
Db 61 SPSFGQVTTISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGYVYHYHGMVWG 110
QY 121 QGTTVTSS 129
Db 111 QGTLVTSS 119

RESULT 5
US-09-025-769B-40
; Sequence 40, Application US/09025769B
; Patent No. 630064

; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-40

Query Match 81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;
QY 1 EVLVQSGAEVKPGESLTKISCKGSGYSFTSYWIGWVRQMPGKLEWMIIPGDSSTRY 60
Db 1 EVLVQSGAEVKPGESLTKISCKGSGYSFTSYWIGWVRQMPGKLEWMIIPGDSSTRY 60
QY 61 SPSFGQATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGYVYHYHGMVWG 120
Db 61 SPSFGQVTTISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGYVYHYHGMVWG 111
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 6
US-09-025-769B-67
; Sequence 67, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373


```

CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKGLWNGIIPGDSSTRY 60
Db 1 EVLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKGLWNGIIPGDSSTRY 60
QY 61 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGVYHYHGMVDWG 120
Db 61 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGVYHYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 7
US-09-490-070A-40
; Sequence 40, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/09/490,070A
APPLICATION NUMBER: 95 11 3021.0
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-070A-40

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKGLWNGIIPGDSSTRY 60
Db 1 EVLVQSGAEVKKPGESLKISCKGSGYSTSYWIGVROMPGKGLWNGIIPGDSSTRY 60
QY 61 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGVYHYHGMVDWG 120
Db 61 SPSPGQQTISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGVYHYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 8
US-09-490-070A-67
; Sequence 67, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

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;
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Colin G. Sandercock, Esq.
;   REGISTRATION NUMBER: 31,298
;   REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 912-2000
;   TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVOSGAEVKKPGESLKISKCKSGYSFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
Db 1 EVLVOSGAEVKKPGESLKISKCKSGYSFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
QY 61 SPSPFOQATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
Db 61 SPSPFOQATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 9
US-09-490-153-40
; Sequence 40, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TELECOMMUNICATION INFORMATION:

;
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Colin G. Sandercock, Esq.
;   REGISTRATION NUMBER: 31,298
;   REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 912-2000
;   TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-070A-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVLVOSGAEVKKPGESLKISKCKSGYSFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
Db 1 EVLVOSGAEVKKPGESLKISKCKSGYSFTSYWIGVROMPGKLEWNGIIPGSDTRY 60
QY 61 SPSPFOQATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
Db 61 SPSPFOQATISADKSIISTAYLOWSSLKASDTAMYICARHVDVGATIGGYIYYHGMVDWG 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 10
US-09-490-153-67
; Sequence 67, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 120 amino acids
;   TYPE: amino acid
;   TELECOMMUNICATION INFORMATION:
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-153-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 60
Db 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 60
QY 61 SPSPGQATISADKSIKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 120
Db 61 SPSPGQATISADKSIKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 11
US-09-490-324-40
; Sequence 40, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-490-324-40

Query Match      81.8%; Score 571.5; DB 2; Length 120;

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Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 60
Db 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 60
QY 61 SPSPGQATISADKSIKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 120
Db 61 SPSPGQATISADKSIKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 120
QY 121 QGTTVTSS 129
Db 112 QGTLVTSS 120

RESULT 12
US-09-490-324-67
; Sequence 67, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-490-324-67

Query Match      81.8%; Score 571.5; DB 2; Length 120;
Best Local Similarity 86.8%; Pred. No. 2.7e-47;
Matches 112; Conservative 1; Mismatches 7; Indels 9; Gaps 2;

QY 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 60
Db 1 EVQLVQSGAEVKPGESLKISKSGSYFTSYWIGWVRQMPGKGLWNGIIPGDSSTRY 60

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QY 61 SPSFQOATISADKSIATAYLOWSSLSKASDTAMYYCARHVDVGCATIGGYIIYHGMVDWG 120
Db 61 SPSFQOQVITISADKSIATAYLOWSSLSKASDTAMYYCARW-----GGDGFY--AMDYWG 111
QY 121 QGTLTVTVSS 129
Db 112 QGTLTVTVSS 120

RESULT 13
US-08-665-202-33
; Sequence 33, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-33

Query Match 74.2%; Score 519; DB 1; Length 98;
Best Local Similarity 99.0%; Pred. No. 2.3e-42;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIIPGSDTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIIPGSDTRY 60
QY 61 SPSFQOATISADKSIATAYLOWSSLSKASDTAMYYCAR 98
Db 61 SPSFQOQVITISADKSIATAYLOWSSLSKASDTAMYYCAR 98

RESULT 14
US-09-315-574-33
; Sequence 33, Application US/09315574

; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-33

Query Match 74.2%; Score 519; DB 2; Length 98;
Best Local Similarity 99.0%; Pred. No. 2.3e-42;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIIPGSDTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIIPGSDTRY 60
QY 61 SPSFQOATISADKSIATAYLOWSSLSKASDTAMYYCAR 98
Db 61 SPSFQOQVITISADKSIATAYLOWSSLSKASDTAMYYCAR 98

RESULT 15
US-10-194-975-45
; Sequence 45, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-45

Query Match	74.2%	Score 519;	DB 2;	Length 98;
Best Local Similarity	99.0%	Pred. No. 2.3e-42;		
Matches 97;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

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Db	1	EVQLVQSGAEVKKPGESLKISCKSGSYFTSYWIGWVRQMPGKLEWNGIIYPGDSITRY	60
QY	61	SPSFGQVTISADKSIISTAYLQWSSLKASDTAMYICAR	98
Db	61	SPSFGQVTISADKSIISTAYLQWSSLKASDTAMYICAR	98

Search completed: April 25, 2007, 04:08:30
Job time : 17.2161 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 48 Seconds
(without alignments)
1251.741 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVLVQSGAEVKKPGESLK1.....YYYYHGMVWGQTTVTSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699	100.0	129	4	US-10-041-860-29
2	699	100.0	129	4	US-10-041-860-215
3	699	100.0	129	4	US-10-041-860-250
4	699	100.0	129	4	US-10-041-860-319
5	699	100.0	129	4	US-10-041-860-319
6	603	86.3	125	5	US-10-665-383-38
7	598.5	85.6	126	4	US-10-041-860-313
8	593.5	84.9	126	4	US-10-041-860-27
9	593.5	84.9	126	4	US-10-041-860-214
10	593.5	84.9	126	4	US-10-041-860-249
11	593.5	84.9	126	4	US-10-665-383-34
12	592.5	84.8	126	4	US-10-041-860-23
13	592.5	84.8	126	4	US-10-041-860-248
14	592.5	84.8	126	4	US-10-041-860-300
15	592.5	84.8	126	4	US-10-665-383-26
16	590	84.4	118	5	US-10-726-332-143
17	589.5	84.3	126	4	US-10-041-860-35
18	589.5	84.3	126	4	US-10-041-860-216
19	589.5	84.3	126	4	US-10-041-860-251
20	589.5	84.3	126	4	US-10-041-860-337
21	589.5	84.3	126	4	US-10-665-383-50
22	587	84.0	118	5	US-10-726-332-3
23	585	83.7	118	5	US-10-726-332-139
24	584	83.5	118	5	US-10-726-332-13
25	584	83.5	118	5	US-10-726-332-140
26	580	83.0	118	5	US-10-726-332-29
27	578	82.7	119	5	US-10-834-397-26

28	576.5	82.5	226	4	US-10-128-520-159	Sequence 159, App
29	576	82.4	252	3	US-09-880-748-1537	Sequence 1537, App
30	576	82.4	252	4	US-10-293-418-1537	Sequence 1537, App
31	576	82.4	252	6	US-11-054-515-1537	Sequence 1537, App
32	576	82.4	252	6	US-11-266-444-1537	Sequence 1537, App
33	573.5	82.0	224	4	US-10-128-520-180	Sequence 180, App
34	573	82.0	118	5	US-10-726-332-145	Sequence 145, App
35	572.5	81.9	116	5	US-10-727-155-100	Sequence 100, App
36	572.5	81.9	222	4	US-10-128-520-169	Sequence 169, App
37	571.5	81.8	120	4	US-10-125-687-6	Sequence 6, Appli
38	571.5	81.8	120	5	US-10-996-191-6	Sequence 6, Appli
39	571.5	81.8	120	5	US-10-834-397-40	Sequence 40, Appl
40	571.5	81.8	120	5	US-10-834-397-67	Sequence 67, Appl
41	571.5	81.8	126	4	US-10-041-860-46	Sequence 46, Appl
42	571.5	81.8	126	4	US-10-041-860-217	Sequence 217, App
43	571.5	81.8	126	4	US-10-041-860-366	Sequence 366, App
44	571.5	81.8	126	4	US-10-665-383-70	Sequence 70, Appl
45	569.5	81.5	224	4	US-10-128-520-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-041-860-29
; Sequence 29, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-29

Query Match 100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVROMPKGLEWGIYPGDSSTRY	60
DB	1	EVLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGVROMPKGLEWGIYPGDSSTRY	60
QY	61	SPSFQQAATISADKSIATAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMVWG	120
DB	61	SPSFQQAATISADKSIATAYLQWSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMVWG	120
QY	121	QGTITVTSS	129
DB	121	QGTITVTSS	129

RESULT 2
US-10-041-860-215
; Sequence 215, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi

```

; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-215

Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
DB 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 3
US-10-041-860-250
; Sequence 250, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-250

Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
DB 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

US-10-041-860-319
; Sequence 319, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-319

Query Match      100.0%; Score 699; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
DB 1 EVQLVQSGAEVKPGESLKISCKGSGYSTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
QY 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
DB 61 SPSPGQATISADKSIATAYLQWSSLKASDTAMYCARHVDVGATIGGYYHYHGMVDVWG 120
QY 121 QGTTVTVSS 129
DB 121 QGTTVTVSS 129

RESULT 5
US-10-665-383-38
; Sequence 38, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRoche, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-38

```



```
RESULT 9
US-10-041-860-214
; Sequence 214, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-214

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY      1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
      |||
Db      1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
      |||

QY      61 SPSFQCGQATISADKSIKTAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
      |||
Db      61 SPSFQCGQATISADKSIKTAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
      |||

QY      117 DWVGQGTVTVTSS 129
      |||
Db      114 DWVGQGTTLVTSS 126
      |||

RESULT 11
US-10-665-383-34
; Sequence 34, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: Larochele, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-34

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY      1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
      |||
Db      1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
      |||

QY      61 SPSFQCGQATISADKSIKTAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
      |||
Db      61 SPSFQCGQATISADKSIKTAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
      |||

QY      117 DWVGQGTVTVTSS 129
      |||
Db      114 DWVGQGTTLVTSS 126
      |||

RESULT 12
US-10-041-860-23
; Sequence 23, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-249

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY      1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
      |||
Db      1 EVQLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWNGIYPGDSSTRY 60
      |||

QY      61 SPSFQCGQATISADKSIKTAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
      |||
Db      61 SPSFQCGQATISADKSIKTAYLOWSSLSKASDTAMYCARHVDVGATIGGYYY----YHGM 116
      |||

QY      117 DWVGQGTVTVTSS 129
      |||
Db      114 DWVGQGTTLVTSS 126
      |||

RESULT 10
US-10-041-860-249
; Sequence 249, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-249

Query Match      84.9%; Score 593.5; DB 4; Length 126;
Best Local Similarity 85.7%; Pred. No. 7.8e-46;
Matches 114; Conservative 1; Mismatches 7; Indels 11; Gaps 2;
```



```
Db      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
61 SPSFOGQVTISADKSI TAYLOWSSILKASDTAMYCARHV-----SYYYVSGSYNVF 113
Qy      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
117 DWMGOGTTVTSS 129
Db      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
114 DWMGOGTLVTSS 126
```

Search completed: April 25, 2007, 04:22:49
Job time : 48.7373 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 50 Seconds
(without alignments)
533.620 Million cell updates/sec

Title: US-10-665-383-38

Perfect score: 699

Sequence: 1 EVQLVQSGAEVKPKGSLK.....YYYYHGMVWGQTTVTSS 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New.*

- 1: /EMC_Celerra_SID33/ptodata/1/pubpaa/US08_NEW_PUB.pdb.*
- 2: /EMC_Celerra_SID33/ptodata/1/pubpaa/US06_NEW_PUB.pdb.*
- 3: /EMC_Celerra_SID33/ptodata/1/pubpaa/US07_NEW_PUB.pdb.*
- 4: /EMC_Celerra_SID33/ptodata/1/pubpaa/US09_NEW_PUB.pdb.*
- 5: /EMC_Celerra_SID33/ptodata/1/pubpaa/US09_NEW_PUB.pdb.*
- 6: /EMC_Celerra_SID33/ptodata/1/pubpaa/US10_NEW_PUB.pdb.*
- 7: /EMC_Celerra_SID33/ptodata/1/pubpaa/US11_NEW_PUB.pdb.*
- 8: /EMC_Celerra_SID33/ptodata/1/pubpaa/US60_NEW_PUB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	699	100.0	129	7	US-11-109-181-29
2	699	100.0	129	7	US-11-109-181-215
3	699	100.0	129	7	US-11-109-181-250
4	699	100.0	129	7	US-11-109-181-319
5	614	87.8	121	7	US-11-440-728-10
6	613.5	87.8	118	7	US-11-440-728-143
7	608	87.0	121	7	US-11-440-728-22
8	608	87.0	121	7	US-11-440-728-145
9	607	86.8	121	7	US-11-440-728-18
10	602	86.1	121	7	US-11-440-728-106
11	602	86.1	121	7	US-11-440-728-118
12	599	85.7	121	7	US-11-440-728-90
13	598.5	85.6	126	7	US-11-109-181-313
14	598	85.6	119	7	US-11-440-728-146
15	598	85.6	121	7	US-11-440-728-98
16	597.5	85.5	124	7	US-11-440-728-6
17	597	85.4	121	7	US-11-440-728-130
18	596	85.3	121	7	US-11-440-728-38
19	595.5	85.2	122	7	US-11-440-728-46
20	595	85.1	121	7	US-11-440-728-151
21	594	85.0	121	7	US-11-440-728-74
22	593.5	84.9	126	7	US-11-109-181-27
23	593.5	84.9	126	7	US-11-109-181-214
24	593.5	84.9	126	7	US-11-109-181-249
25	592.5	84.8	126	7	US-11-109-181-23

ALIGNMENTS

RESULT 1

US-11-109-181-29
; Sequence 29, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Biryam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18.
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-29

Query Match 100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EVQLVQSGAEVKPKGSLKISCKGSGYSFTSYWIGVWRQMPKGLWNGIIPGDSSTRY	60
Db	1	EVQLVQSGAEVKPKGSLKISCKGSGYSFTSYWIGVWRQMPKGLWNGIIPGDSSTRY	60
Qy	61	SPSFQQTATISADKSIISTAYLQSSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMVWG	120
Db	61	SPSFQQTATISADKSIISTAYLQSSSLKASDTAMYYCARHVDVGATIGGYYYYYHGMVWG	120
Qy	121	QGTVTVTSS	129
Db	121	QGTVTVTSS	129

RESULT 2

US-11-109-181-215
; Sequence 215, Application US/11109181

```

; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-215

Query Match      100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60

QY 61 SPSFQQAATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120
Db 61 SPSFQQAATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120

QY 121 QGTTVTVSS 129
Db 121 QGTTVTVSS 129

RESULT 4
US-11-109-181-319
; Sequence 319, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-319

Query Match      100.0%; Score 699; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60
Db 1 EVQLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDSSTRY 60

QY 61 SPSFQQAATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120
Db 61 SPSFQQAATISADKSIISTAYLQWSSLKASDTAMYYCARHVDVGATIGGYYHYHGMVDWG 120

QY 121 QGTTVTVSS 129
Db 121 QGTTVTVSS 129

RESULT 5
US-11-440-728-10
; Sequence 10, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USRS
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728

```

```
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2006-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 121
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-440-728-10

Query Match      87.8%; Score 614; DB 7; Length 121;
Best Local Similarity 89.9%; Pred. No. 8.5e-50;
Matches 116; Conservative 2; Mismatches 3; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||

QY 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 120
   |||||
Db 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 112
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 113 QGTTVTSS 121

RESULT 6
US-11-440-728-143
; Sequence 143, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2006-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 118
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-440-728-143

Query Match      87.8%; Score 613.5; DB 7; Length 118;
Best Local Similarity 89.9%; Pred. No. 9.3e-50;
Matches 116; Conservative 1; Mismatches 1; Indels 11; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||

QY 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 120
   |||||
Db 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 109
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 110 QGTTVTSS 118

RESULT 7
US-11-440-728-22
; Sequence 22, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2006-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 121
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-440-728-145

Query Match      87.0%; Score 608; DB 7; Length 121;
Best Local Similarity 91.5%; Pred. No. 3.1e-49;
Matches 118; Conservative 1; Mismatches 2; Indels 8; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||

QY 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 120
   |||||
Db 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 112
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 113 QGTTVTSS 121

RESULT 8
US-11-440-728-145
; Sequence 145, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR FILING DATE: 2006-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 121
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-440-728-145

Query Match      87.0%; Score 608; DB 7; Length 121;
Best Local Similarity 91.5%; Pred. No. 3.1e-49;
Matches 118; Conservative 1; Mismatches 2; Indels 8; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYFTSYWIGWVRQMPGKGLWGMGIIPGDS DTRY 60
   |||||

QY 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 120
   |||||
Db 61 SPSPQOATISADKSIATAYLQWSSLSKASDTAMYCARHVDVGATIGGYYHYHGM DVMG 112
   |||||

QY 121 QGTTVTSS 129
   |||||
Db 113 QGTTVTSS 121
```

```

db      61 SPSPGQQTIVISADKSIISTAYLQWSSLKASDTAMYYCAR---VGAT-----NTTYGMDVWG 112
Qy      121 QGTTVTYVSS 129
db      113 QGTTVTYVSS 121

```

RESULT 9

```

US-11-440-728-18
; Sequence 18, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-18

```

RESIT.T 10

```

RESULI 10
US-11-440-728-106
; Sequence 106, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-11-440-728-106

Query Match	86.1%;	Score 602;	DB 7;	Length 121;
Best Local Similarity	89.8%;	Pred. No. 1.1e-48;		
Matches 115;	Conservative 0;	Mismatches 5;	Indels 8;	Gaps 1;
Qy	2	VQLVQSGAEVKKPGESLKISKCKSGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGSDSDTRY	61	
Db	2	VQLVQSGAEVKKPGESLKISKCKSGSGYSTSYWIGVWRQMPGKGLWMMGIIYPGSDSDTRY	61	
Qy	62	PSFGQATISADKSIISTAYLQWSLKSADTAMYYCARHVDVGATIGSGYYYYYHGMVDWGQ	121	
Db	62	PSFGQVIISADKSIISTAYLQWSLKSADTAMYYCAR-----TGDIYSYHGMDVWGQ	113	
Qy	122	GTTVTWSS	129	
Db	114	GTTVTWSS	121	

RESULT 11

```

US-11-440-728-118
; Sequence 118, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEV, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-118

```

RESULT 12

RESUL 12
US-11-440-728-90
; Sequence 90, Application US/11440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; TITLE OF INVENTION: THEREOF

```
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-90

Query Match      85.7%; Score 599; DB 7; Length 121;
Best Local Similarity 88.4%; Pred. No. 2.1e-48;
Matches 114; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDS DTRY 60
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDS DTRY 60
QY 61 SPSFQQTATISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYHYHGM DVMG 120
Db 61 SPSFQQTATISADKSI RTAYLQWSSLKASDTAMYICARHVDVGCATIGGYYHYHGM DVMG 112
QY 121 QGTTVTVSS 129
Db 113 QGTTVTVSS 121

RESULT 13
US-11-109-181-313
; Sequence 313, Application US/11/109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvelan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-313

Query Match      85.6%; Score 598.5; DB 7; Length 126;
Best Local Similarity 86.5%; Pred. No. 2.5e-48;
Matches 115; Conservative 1; Mismatches 6; Indels 11; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDS DTRY 60
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDS DTRY 60
QY 61 SPSFQQTATISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYHYHGM 116
Db 61 SPSFQQTATISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYHYHGM 113
QY 117 DWGQGTVTVSS 129
Db 114 DWGQGTVTVSS 126
```

```
RESULT 14
US-11-440-728-146
; Sequence 146, Application US/11/440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-146

Query Match      85.6%; Score 598; DB 7; Length 119;
Best Local Similarity 89.9%; Pred. No. 2.6e-48;
Matches 116; Conservative 0; Mismatches 3; Indels 10; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDS DTRY 60
Db 1 EVOLVQSGAEVKKPGESLKISCKGSGYSTSYWIGWVRQMPGKLEWNGIIPGDS DTRY 60
QY 61 SPSFQQTATISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYHYHGM DVMG 120
Db 61 SPSFQQTATISADKSI STAYLQWSSLKASDTAMYICARHVDVGCATIGGYYHYHGM DVMG 110
QY 121 QGTTVTVSS 129
Db 111 QGTTVTVSS 119
```

```
RESULT 15
US-11-440-728-98
; Sequence 98, Application US/11/440728
; Publication No. US20070014720A1
; GENERAL INFORMATION:
; APPLICANT: GAZIT-BORNSTEIN, Gadi
; APPLICANT: GREEN, Larry L.
; APPLICANT: YANG, Xiaodong
; APPLICANT: QUEVA, Christophe
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO CD20 AND USES
; FILE REFERENCE: ABXAZ.003A
; CURRENT APPLICATION NUMBER: US/11/440,728
; CURRENT FILING DATE: 2006-05-25
; PRIOR APPLICATION NUMBER: US 60/686,992
; PRIOR FILING DATE: 2005-06-02
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-440-728-98

Query Match      85.6%; Score 598; DB 7; Length 121;
Best Local Similarity 87.6%; Pred. No. 2.6e-48;
Matches 113; Conservative 3; Mismatches 5; Indels 8; Gaps 1;
```



```
QY 1 EVQLVQSGAEVKKPESLKISKKGSGYSFTSYWICWVRQMPGKGLEWNGIIPGSDTRY 60
Db 1 EVQLVQSGAEVKKPESLKISKKGSGYSFTSYWICWVRQMPGKGLEWNGIIPGSDTRY 60
QY 61 SPSPGQGTISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 120
Db 61 SPSPGQGTISADKSIISTAYLQWSSLKASDTAMYICARHVDVGATIGGYYHYHGMVWG 112
QY 121 QGTTVTVSS 129
Db 113 QGTTVTVSS 121
```

Search completed: April 25, 2007, 04:27:43
Job time : 49.7415 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:54:56 ; Search time 98 Seconds
(without alignments)
564.248 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSPISLPLVTECPAS.....MQALQSLMCSFGQTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 48933398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_200701.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*
- 11: Geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	113	7	ADK18831
2	590	100.0	113	7	ADK18797
3	590	100.0	113	7	ADK18606
4	590	100.0	113	8	ADL25430
5	576.5	97.7	114	7	ADK18898
6	556	94.2	248	4	AGG65590
7	555	94.1	113	3	AAV95221
8	554.5	94.0	131	10	AEJ57801
9	554.5	94.0	146	10	AEJ57944
10	554	93.9	113	3	AAV95220
11	554	93.9	113	8	ADL22126
12	554	93.9	114	3	AAV95186
13	554	93.9	131	3	AAV95226
14	550	93.2	112	8	ADP47300
15	550	93.2	223	10	AEK98277
16	550	93.2	223	10	AEK98219
17	549	93.1	113	8	ADL22125
18	548.5	93.0	110	7	ADP03295
19	548.5	93.0	112	8	ADL22111
20	547.5	92.8	112	8	ADL22129
21	547.5	92.8	112	8	ADL22112
22	547	92.7	111	3	AAV95225

23	547	92.7	112	3	AAV95187	Aay95187 Anti-plat
24	547	92.7	112	8	ADP47109	Adp47109 Human pho
25	547	92.7	112	9	AEA45169	Aea45169 Apolipopr
26	547	92.7	113	10	AEJ64254	Aej64254 Human ant
27	546.5	92.6	112	8	ADL22114	Adl22114 Anti-plat
28	546.5	92.6	112	10	AEH82673	Aeh82673 Human ant
29	546.5	92.6	112	10	AEI93626	Aei93626 Human lig
30	546.5	92.6	112	10	AEJ42800	Aej42800 IGF-R ant
31	546.5	92.6	112	10	AEJ42864	Aej42864 IGF-R ant
32	546.5	92.6	112	10	AEJ42818	Aej42818 IGF-R ant
33	546.5	92.6	112	10	AEK41374	Aek41374 Human imm
34	546.5	92.6	113	10	AEH82663	Aeh82663 Human ant
35	546.5	92.6	113	10	AEI65178	Aei65178 Anti-Ang-
36	546.5	92.6	115	10	AEH82634	Aeh82634 Human ant
37	546.5	92.6	115	10	AEH82642	Aeh82642 Human ant
38	546.5	92.6	115	10	AEH82626	Aeh82626 Human ant
39	546.5	92.6	115	10	AEH82618	Aeh82618 Human ant
40	546.5	92.6	134	9	ADV67311	Adv67311 Amino aci
41	546.5	92.6	134	10	AEI42744	Aei42744 Human imm
42	546.5	92.6	134	10	AEI62909	Aei62909 Human ant
43	546	92.5	111	8	ADP22370	Adp22370 Human ant
44	546	92.5	112	8	ADP46986	Adp46986 Murine li
45	545.5	92.5	112	7	ADJ76892	Adj76892 Anti-IGF-

ALIGNMENTS

RESULT 1
ADK18831
ID ADK18831 standard; protein; 113 AA.
AC ADK18831;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #57.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 255; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.

```
XX SQ Sequence 113 AA;
Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113
DB 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113

RESULT 2
ADK18797
ID ADK18797 standard; protein; 113 AA.
XX
AC ADK18797;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody protein related sequence #23.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 221; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113
DB 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113

RESULT 3
ADK18606
ID ADK18606 standard; protein; 113 AA.
XX
AC ADK18606;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody light chain protein sequence.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 30; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113
DB 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113

RESULT 4
ADL25430
ID ADL25430 standard; protein; 113 AA.
XX
AC ADL25430;
XX
DT 17-JUN-2004 (first entry)
XX
```

```
XX SQ Sequence 113 AA;
Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113
DB 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113

RESULT 3
ADK18606
ID ADK18606 standard; protein; 113 AA.
XX
AC ADK18606;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody light chain protein sequence.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 30; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113
DB 61 SGVPRFSGSGGTDTLTKISRVEADDVGYYCQALQSLMCSFGQGTKEIK 113

RESULT 4
ADL25430
ID ADL25430 standard; protein; 113 AA.
XX
AC ADL25430;
XX
DT 17-JUN-2004 (first entry)
XX
```

DE Human mAb 1.29 light chain variable region protein SEQ ID NO:40.
XX antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW gene therapy; human; monoclonal antibody; mAb.
XX
OS Homo sapiens.
XX
PN WO2004024098-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029414.
XX
PR 16-SEP-2002; 2002US-0411137P.
XX
XX (ABGE-) ABGENIX INC.
PA (CURA-) CURAGEN CORP.
XX
PI Floege J, Garit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;
XX WPI; 2004-269881/25.
DR N-PSDB; ADL25429.
DR
XX
XX Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.
PT
XX
XX Disclosure; SEQ ID NO 40; 115pp; English.
PS
XX
CC The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 113 AA;
SQ
Query Match 100.0%; Score 590; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLRKPGSQPLLIIYLGSNRA 60
DB 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLRKPGSQPLLIIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEADDDVGYVYCMQALQSLMCSFGGQTKLEIK 113
DB 61 SGVPDRFSGSGGTFTLKISRVEADDDVGYVYCMQALQSLMCSFGGQTKLEIK 113
RESULT 5
ADK18898
ID ADK18898 standard; protein; 114 AA.
XX
XX ADK18898;
XX
XX
DT 06-MAY-2004 (first entry)
DE
DE Anti-human PDGF-D antibody protein related sequence #124.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX

OS Homo sapiens.
XX WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
XX (ABGE-) ABGENIX INC.
PA
XX Corvalan JRF, Jia X, Peng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
XX WPI; 2003-587119/55.
DR
XX New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
PT
XX
PS Disclosure; SEQ ID NO 322; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC useful for modulating collagen formation, and for staging various
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC generated using an active protein fragment of the gene product from the
CC clone 30664188.0.99 arising in the conditioned medium obtained when
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC sequence corresponds to a protein used in the invention.
XX
XX Sequence 114 AA;
SQ
Query Match 97.7%; Score 576.5; DB 7; Length 114;
Best Local Similarity 98.2%; Pred. No. 4.6e-42;
Matches 112; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLRKPGSQPLLIIYLGSNRA 60
DB 1 DIVMTQSLPLPVTGEPASISCRSSQSLHSHNGYNYLDWYLRKPGSQPLLIIYLGSNRA 60
QY 61 SGVPDRFSGSGGTFTLKISRVEADDDVGYVYCMQALQSLMCSFGGQTKLEIK 113
DB 61 SGVPDRFSGSGGTFTLKISRVEADDDVGYVYCMQALQSLMCSFGGQTKLEIK 114
RESULT 6
AAG65590
ID AAG65590 standard; protein; 248 AA.
XX
XX AAG65590;
XX
XX
DT 07-JAN-2002 (first entry)
XX
XX Anti-hEDRF antibody e9 amino acid sequence.
DE
XX Human; erythroid differentiation related factor; hEDRF; antianemic;
KW erythrocyte deficiency; antibody e9.
XX
XX Homo sapiens.
OS
XX EP1130030-A1.
PN
XX
XX
PD 05-SEP-2001.
XX
XX 27-FEB-2001; 2001EP-00104821.
PF
XX
XX 02-MAR-2000; 2000US-00517225.
PR
XX
XX (HOFF) ROCHE DIAGNOSTICS CORP.
PA

XX Xu H, Mahoney W, Schueler P, Harriman WD;
 XX WPI; 2001-608195/70.
 DR N-PSDB; AAH47762.
 XX Novel human erythroid differentiation related factor and polynucleotides
 PT encoding it useful for treating anemia and other erythrocyte deficiencies
 PT and for detecting expression of the factor in humans.
 XX Disclosure; Fig 4; 29pp; English.
 XX The invention provides a human erythroid differentiation related factor
 CC (hEDRF). The hEDRF polypeptide and the encoding polynucleotide are useful
 CC for treating anemias and other erythrocyte deficiencies. The hEDRF
 CC protein is useful for producing antibodies, useful in screening assays to
 CC identify pharmaceutical compounds of interest and compounds which bind to
 CC hEDRF. The polynucleotides are useful for producing hEDRF or its related
 CC polypeptides. The antibodies are useful for separating or detecting the
 CC corresponding antigen e.g. for detection/quantitation of hEDRF in samples
 CC taken from human subjects. Quantification of hEDRF at immunohistochemical
 CC level finds value in evaluating the potential of the tissue site to
 CC contribute towards the production of new erythroid cells. The present
 CC sequence represents the amino acid sequence of an anti-hEDRF antibody e9
 XX Sequence 248 AA;
 SQ
 Query Match 94.2%; Score 556; DB 4; Length 248;
 Best Local Similarity 93.8%; Pred. No. 6.1e-40;
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNVLDWYLOKPGQSPQLLIYLGSNRA 60
 DB 135 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNVLDWYLOKPGQSPQLLIYLGSNRA 194
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113
 DB 195 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 247
 RESULT 7
 AA95221
 ID AA95221 standard; protein; 113 AA.
 AC AA95221;
 DT 29-AUG-2000 (first entry)
 XX Anti-platelet glycoprotein Ib human HIB-5 VL.
 XX Variable light chain; single chain antibody; scFv; human; HIB-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Region 1..23
 FT /note= "framework region 1"
 FT Region 24..39
 FT /note= "complementarity determining region 1"
 FT Region 40..54
 FT /note= "framework region 2"
 FT Region 55..61
 FT /note= "complementarity determining region 2"
 FT Region 62..93
 FT /note= "framework region 3"
 FT Region 94..101
 FT /note= "complementarity determining region 3"
 FT Region 102..113
 FT /note= "framework region 4"
 XX WO200026667-A1.

XX 11-MAY-2000.
 PD 29-OCT-1999; 99WO-US025495.
 XX 30-OCT-1998; 98US-0106275P.
 PR (MILL/) MILLER J L.
 PA Miller JL;
 PI WPI; 2000-365744/31.
 DR Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 XX Ib alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.
 PT Claim 18; Fig 8; 89pp; English.
 PS The present sequence is that of the light chain variable region (VL) of
 CC human single chain antibody (scFv) HIB-5, which is directed against
 CC platelet glycoprotein Ib (GPIb). The HIB series of scFv was isolated from
 CC a human synthetic VH and VL scFv library by 3 rounds of phagemid
 CC selection against transfected CHO cells expressing the GPIb alpha
 CC component of the GPIb/IX/V complex on their surface, followed by a 4th
 CC round of selection against washed human platelets, and 2 final rounds in
 CC which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AA95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by Escherichia coli, the HIB scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIb alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Note: The present sequence is
 CC not shown in the specification but is derived from the HIB-5 VH sequence
 CC given in Fig 8 (see AA95220)
 XX Sequence 113 AA;
 SQ
 Query Match 94.1%; Score 555; DB 3; Length 113;
 Best Local Similarity 94.7%; Pred. No. 3.2e-40;
 Matches 107; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNVLDWYLOKPGQSPQLLIYLGSNRA 60
 DB 1 DIVMTQSPPLSLPVTPGEPASISCRSSQSLHSHNGYNVLDWYLOKPGQSPQLLIYLGSNRA 60
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113
 DB 61 SGVPRFSGSGGTDFTLKISRVEADGVVYCMQALQSLMCSFGQGTGLEIK 113
 RESULT 8
 AEJ57801
 ID AEJ57801 standard; protein; 131 AA.
 XX AEJ57801;
 AC AEJ57801;
 DT 05-OCT-2006 (first entry)
 XX Human antibody enzyme V-kappa2 VL PHVK-1 #1, SEQ.4.
 DE Abzyme; antibody; immunoglobulin; infection; antimicrobial; cancer;
 KW cytostatic; diagnostic; peptidase; light chain variable region; enzyme.
 OS Homo sapiens.
 XX JP2006197930-A.

```

XX PD 03-AUG-2006.
XX PF 22-DEC-2005; 2005JP-00370880.
XX PR 22-DEC-2004; 2004JP-00372206.
XX PA (HIRO-) HIROSHIMA KEN.
XX PI Uda T, Hifumi M;
XX DR WPI; 2006-544634/56.
XX DR N-PSDB; AEJ57944.
XX PT New human enzyme antibody consisting of light chain or heavy chain
XX PT polypeptides encoded by human germ line gene e.g. L22 and VH1-24, useful
XX PT for treatment and diagnosis of infectious diseases and cancer.
XX PS Claim 5; SEQ ID NO 4; 30pp; Japanese.
XX CC The invention relates to a human antibody enzyme (abzyme) having high
XX CC recognition ability and high enzyme activity. The antibody enzyme
XX CC comprises a light chain encoded by a human germ line gene selected from
XX CC L22, V1-9, V1-13, V1-18, V1-22, V2-6, V2-7, V2-8, V2-13, V2-14, V3-3, A1,
XX CC A2, A3, A5, A7, A10, A17, A18, A19, A23, A26, A30, L14 and L22, and a
XX CC heavy chain encoded by a human germ line gene selected from VH1-24, VH3-
XX CC 9, VH3-13, VH3-16, VH3-20, VH3-30, VH3-33, VH3-43, VH3-64, VH3-
XX CC 72, VH3-73, VH3-74, VH4-34 and VH7-81. The invention also relates to a
XX CC method for producing a human antibody enzyme belonging to a particular
XX CC subgroup involving selection of human lymphocyte cDNAs encoding an
XX CC antibody with enzymatic activity using a primer based on a subgroup-
XX CC specific sequence. The antibody enzymes of the invention can be used in a
XX CC variety of fields, such as the medical industry, pharmaceutical industry,
XX CC reagent industry, medical equipment industry or food industry. The
XX CC antibody enzymes are useful in the diagnosis and treatment of medical
XX CC conditions such as cancer and various infectious diseases, and can also
XX CC be used in biosensors and biomaterials. The antibody enzymes exhibit high
XX CC in vivo efficacy for therapeutic applications, and can be produced
XX CC efficiently. The present sequence represents a specifically claimed V-
XX CC kappa2 light chain variable region (VL) of a human antibody enzyme having
XX CC peptidase activity. This sequence comprises a Ser-His-Asp (S-H-D)
XX CC catalytic triad. Note: The present sequence is shown in the sequence
XX CC listing of the specification and differs from the sequence also referred
XX CC to as VL pHVK-1 (AEJ57944) which is shown in Figure 18.
XX SQ Sequence 131 AA;
Query Match 94.0%; Score 554.5; DB 10; Length 131;
Best Local Similarity 95.6%; Pred. No. 4.2e-40;
Matches 108; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 DIVMTQSLPLVPTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 60
DB 1 DIVMTQSLPLVPTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEADDVGVYVCMAQLQSLMCSFGQGTGLEIK 113
DB 61 SGVPDRFSGSGGTDFTLKISRVEADDVGVYVCMAQLQSLMCSFGQGTGLEIK 112
RESULT 9
AEJ57944
ID AEJ57944 standard; protein; 146 AA.
XX AC AEJ57944;
XX DT 05-OCT-2006 (first entry)
XX DE Human antibody enzyme V-kappa2 VL pHVK-1 #2.
XX KW Abzyme; antibody; immunoglobulin; infection; antimicrobial; cancer;
XX KW cytostatic; diagnostic; peptidase; light chain variable region; enzyme.
OS Homo sapiens.
XX JF2006197930-A.
XX PD 03-AUG-2006.
XX PF 22-DEC-2005; 2005JP-00370880.
XX PR 22-DEC-2004; 2004JP-00372206.
XX PA (HIRO-) HIROSHIMA KEN.
XX PI Uda T, Hifumi M;
XX DR WPI; 2006-544634/56.
XX DR N-PSDB; AEJ57943.
XX PT New human enzyme antibody consisting of light chain or heavy chain
XX PT polypeptides encoded by human germ line gene e.g. L22 and VH1-24, useful
XX PT for treatment and diagnosis of infectious diseases and cancer.
XX PS Example 3; Fig 18; 30pp; Japanese.
XX CC The invention relates to a human antibody enzyme (abzyme) having high
XX CC recognition ability and high enzyme activity. The antibody enzyme
XX CC comprises a light chain encoded by a human germ line gene selected from
XX CC L22, V1-9, V1-13, V1-18, V1-22, V2-6, V2-7, V2-8, V2-13, V2-14, V3-3, A1,
XX CC A2, A3, A5, A7, A10, A17, A18, A19, A23, A26, A30, L14 and L22, and a
XX CC heavy chain encoded by a human germ line gene selected from VH1-24, VH3-
XX CC 9, VH3-13, VH3-16, VH3-20, VH3-30, VH3-33, VH3-43, VH3-64, VH3-
XX CC 72, VH3-73, VH3-74, VH4-34 and VH7-81. The invention also relates to a
XX CC method for producing a human antibody enzyme belonging to a particular
XX CC subgroup involving selection of human lymphocyte cDNAs encoding an
XX CC antibody with enzymatic activity using a primer based on a subgroup-
XX CC specific sequence. The antibody enzymes of the invention can be used in a
XX CC variety of fields, such as the medical industry, pharmaceutical industry,
XX CC reagent industry, medical equipment industry or food industry. The
XX CC antibody enzymes are useful in the diagnosis and treatment of medical
XX CC conditions such as cancer and various infectious diseases, and can also
XX CC be used in biosensors and biomaterials. The antibody enzymes exhibit high
XX CC in vivo efficacy for therapeutic applications, and can be produced
XX CC efficiently. The present sequence represents a V-kappa2 light chain
XX CC variable region (VL) of a human antibody enzyme having peptidase
XX CC activity. This sequence comprises a Ser-His-Asp (S-H-D) catalytic triad.
XX CC Note: The present sequence is shown in Figure 18 of the specification and
XX CC differs from the sequence also referred to as VL pHVK-1 (AEJ57801) which
XX CC is shown in the sequence listing.
XX SQ Sequence 146 AA;
Query Match 94.0%; Score 554.5; DB 10; Length 146;
Best Local Similarity 95.6%; Pred. No. 4.7e-40;
Matches 108; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 DIVMTQSLPLVPTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 60
DB 16 DIVMTQSLPLVPTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLIYLGSNRA 75
QY 61 SGVPDRFSGSGGTDFTLKISRVEADDVGVYVCMAQLQSLMCSFGQGTGLEIK 113
DB 76 SGVPDRFSGSGGTDFTLKISRVEADDVGVYVCMAQLQSLMCSFGQGTGLEIK 127
RESULT 10
AAJ95220
ID AAJ95220 standard; protein; 113 AA.
XX AC AAJ95220;
XX DT 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human H1b-5 VL.

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Variable light chain; single chain antibody; scFv; human; H1b-5;
glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
antithrombotic; thrombus; therapy; diagnostic.

Homo sapiens.

Location/Qualifiers

Key
Region 1..23
/note= "framework region 1"
Region 24..39
/note= "complementarity determining region 1"
Region 40..54
/note= "framework region 2"
Region 55..61
/note= "complementarity determining region 2"
Region 62..93
/note= "framework region 3"
Region 94..101
/note= "complementarity determining region 3"
Region 102..113
/note= "framework region 4"

WO200026667-A1.

11-MAY-2000.

29-OCT-1999; 99WO-US025495.

30-OCT-1998; 98US-0106275P.

(MILLER) MILLER J L.

Miller JL;

WPI; 2000-365744/31.

Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
Ib alpha molecule useful for producing antibodies which inhibit platelet
aggregation.

Claim 18; Fig 8; 89pp; English.

The present sequence is that of the light chain variable region (VL) of
human single chain antibody (scFv) H1b-5, which is directed against
platelet glycoprotein Ib (GPIb). The H1b series of scFv was isolated from
a human synthetic VH and VL scFv library by 3 rounds of phagemid
selection against transfected CHO cells expressing the GPIb alpha
component of the GPIb/IX/V complex on their surface, followed by a 4th
round of selection against washed human platelets, and 2 final rounds in
which attempts were made to displace scFv from washed platelets by
flooding with murine monoclonal antibody or mimotope peptide (see
AA95229). Whether displayed as surface proteins on a phagemid or
secreted as free scFv by *Escherichia coli*, the H1b scFv clones are
capable of inhibiting von Willebrand factor-dependent aggregation of
platelets. The scFv are composed of native human protein sequences and
therefore attractive potential reagents for therapeutic purposes.
They provide a new class of antithrombotic agents, useful for the
prevention of platelet-dependent thrombi in diseased arteries, bypass
grafts, dialysis etc., and can also be used as diagnostic reagents.
Methods of inhibiting aggregation of platelets, of binding human platelet
GPIb alpha and of selecting a VH or VL region of an antibody that
inhibits platelet aggregation are claimed

Sequence 113 AA;

Query Match 93.9%; Score 554; DB 3; Length 113;

Best Local Similarity 93.8%; Pred. No. 4e-40;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

1 DIVMTQSLPLSVPTGEPASISCRSSQSLHNGVNYLDWYLOKPGQSPQLLYLGSNRA 60

1 DVVMTQSLPLSVPTGEPASISCRSSQSLHNGVNYLDWYLOKPGQSPQLLYLGSNRA 60

QY

61 SGVPRFSGSGGTFTLKISRVEADVGYYCMQALQSLMCSFGQGTLEIK 113

61 SGVPRFSGSGGTFTLKISRVEADVGYYCMQALQTPFPFTFGQGTLEIK 113

RESULT 11

ADI22126

ID ADI22126 standard; protein; 113 AA.

XX ADI22126;

XX 22-APR-2004 (first entry)

XX Anti-platelet autoantibody related light chain amino acid L50 SEQ:89.

XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;
thrombus; platelet adhesion inhibition;
thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
thrombolytic; human.

XX Homo sapiens.

OS Synthetic.

XX WO2004005890-A2.

XX 15-JAN-2004.

XX 03-JUL-2003; 2003WO-US021304.

XX 03-JUL-2002; 2002US-0394352P.

XX 18-SEP-2002; 2002US-0411694P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

WPI; 2004-142998/14.

N-PSDB; ADI22073.

Claim 12; SEQ ID NO 89; 232pp; English.

The present invention describes a method (M1) for identifying an anti-platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10) inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein Iib/Iiia, where the autoantibody, or its fragment comprises an antigen binding region derived from an H414 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein Iib/Iiia, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing

CC and for developing therapeutics for diseases mediated by autoantibody
 CC binding with platelet antigens. (M6) and (M12) are useful for treating
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood
 CC clotting. The present sequence is used in the exemplification of the
 CC present invention.

XX SQ Sequence 113 AA;
 Query Match 93.9%; Score 554; DB 8; Length 113;
 Best Local Similarity 93.8%; Pred. No. 4e-40; Mismatches 4; Indels 0; Gaps 0;
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYKPKGQSPQLLIYLGSNRA 60
 |||||
 DB 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYKPKGQSPQLLIYLGSNRA 60
 |||||

QY 61 SGVDRFSGSGGTDTLTKISRVEADVGVYCMQALQSLMCSFGQGTLEIK 113
 |||||
 DB 61 SGVDRFSGSGGTDTLTKISRVEADVGVYCMQALQTRPVTFGQGTLEIK 113
 |||||

RESULT 12
 AAY95186
 ID AAY95186 standard; protein; 114 AA.
 XX AC AAY95186;
 XX DT 29-AUG-2000 (first entry)
 XX DE Anti-platelet glycoprotein Ib human H1b-5 VL.
 DE Variable light chain; single chain antibody; scFv; human; H1b-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Region 1..23
 FT /note= "framework region 1"
 FT Region 24..39
 FT /note= "complementarity determining region 1"
 FT Region 40..54
 FT /note= "framework region 2"
 FT Region 55..61
 FT /note= "complementarity determining region 2"
 FT Region 62..93
 FT /note= "framework region 3"
 FT Region 94..101
 FT /note= "complementarity determining region 3"
 FT Region 102..114
 FT /note= "framework region 4"
 XX WO200026667-A1.
 XX PD 11-MAY-2000.
 XX PF 29-OCT-1999; 99WO-US025495.
 XX PR 30-OCT-1998; 98US-0106275P.
 XX PA (MILL/) MILLER J L.
 XX PI Miller JL;
 XX WPI: 2000-365744/31.
 XX N-PSDB; AAA27664.
 XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 PT Ib alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.

PS Claim 11; Page 77; 89pp; English.
 XX The present sequence is that of the light chain variable region (VL) of
 CC human single chain antibody (scFv) H1b-5, which is directed against
 CC platelet glycoprotein Ib (GP1b). The H1b series of scFv was isolated from
 CC a human synthetic VH and VL scFv library by 3 rounds of phagemid
 CC selection against transfected CHO cells expressing the GP1b alpha
 CC component of the GP1b/IX/V complex on their surface, followed by a 4th
 CC round of selection against washed human platelets, and 2 final rounds in
 CC which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AAY95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by *Escherichia coli*, the H1b scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GP1b alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed

XX SQ Sequence 114 AA;
 Query Match 93.9%; Score 554; DB 3; Length 114;
 Best Local Similarity 93.8%; Pred. No. 4e-40; Mismatches 4; Indels 0; Gaps 0;
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYKPKGQSPQLLIYLGSNRA 60
 |||||
 DB 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYKPKGQSPQLLIYLGSNRA 60
 |||||

QY 61 SGVDRFSGSGGTDTLTKISRVEADVGVYCMQALQSLMCSFGQGTLEIK 113
 |||||
 DB 61 SGVDRFSGSGGTDTLTKISRVEADVGVYCMQALQTRPVTFGQGTLEIK 113
 |||||

RESULT 13
 AAY95226
 ID AAY95226 standard; protein; 131 AA.
 XX AC AAY95226;
 XX DT 29-AUG-2000 (first entry)
 XX DE Anti-platelet glycoprotein Ib human H1b-5 VL region and linker.
 DE Variable light chain; single chain antibody; scFv; human; H1b-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 XX OS Synthetic.
 OS Homo sapiens.
 OS Chimeric.

XX FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /note= "vector-derived linker"
 FT Region 18..131
 FT /note= "light chain variable region"
 FT Region 18..40
 FT /note= "framework region 1"
 FT Region 41..56
 FT /note= "complementarity determining region 1"
 FT Region 57..71
 FT /note= "framework region 2"
 FT Region 72..78
 FT /note= "complementarity determining region 2"
 FT Region 79..110
 FT /note= "framework region 3"
 FT Region 111..119
 FT /note= "complementarity determining region 3"

FT Region 120. .131
 /note= "framework region 4"
 FN WO200026667-A1.
 XX 11-MAY-2000.
 PD 29-OCT-1999; 99WO-US025495.
 PF 30-OCT-1998; 98US-0106275P.
 PR (MILL/) MILLER J L.
 XX Miller JL;
 PA WPI; 2000-365744/31.
 DR Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
 PT Ib alpha molecule useful for producing antibodies which inhibit platelet
 PT aggregation.
 XX Disclosure; Fig 8; 89pp; English.
 XX The present sequence is that of the light chain variable region (VL) plus
 CC linker peptide of human single chain antibody (scFv) HIB-5, which is
 CC directed against platelet glycoprotein Ib (GP1b). HIB-5 is composed of a
 CC heavy chain variable region and light chain variable region joined via a
 CC vector-derived peptide linker. The HIB series of scFv was isolated from a
 CC human synthetic VH and VL scFv library by 3 rounds of phagemid selection
 CC against transfected CHO cells expressing the GP1b alpha component of the
 CC GP1b/IX/V complex on their surface, followed by a 4th round of selection
 CC against washed human platelets, and 2 final rounds in which attempts were
 CC made to displace scFv from washed platelets by flooding with murine
 CC monoclonal antibody or mimotope peptide (see AA95229). Whether displayed
 CC as surface proteins on a phagemid or secreted as free scFv by Escherichia
 CC coli, the HIB scFv clones are capable of inhibiting von Willebrand factor
 CC -dependent aggregation of platelets. The scFv are composed of native
 CC human protein sequences and are therefore attractive potential reagents
 CC for therapeutic purposes. They provide a new class of antithrombotic
 CC agents, useful for the prevention of platelet-dependent thrombi in
 CC diseased arteries, bypass grafts, dialysis etc., and can also be used as
 CC diagnostic reagents. Methods of inhibiting aggregation of platelets, of
 CC binding human platelet GP1b alpha and of selecting a VH or VL region of
 CC an antibody that inhibits platelet aggregation are claimed
 XX
 SQ Sequence 131 AA;
 Query Match 93.9%; Score 554; DB 3; Length 131;
 Best Local Similarity 93.8%; Pred. No. 4.6e-40;
 Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
 Db 18 DVVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 77
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVYYCMQALQSLMCSFGQGTGLEIK 113
 Db 78 SGVPRFSGSGGTDFTLKISRVEADGVYYCMQALQTPPTFGQGTGLEIK 130
 RESULT 14
 ADP47300
 ID ADP47300 standard; protein; 112 AA.
 XX ADP47300;
 AC ADP47300;
 XX
 DT 09-SEP-2004 (first entry)
 DE Human phospholipase A2-specific monoclonal antibody light chain #20.
 XX human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;

KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
 OS Homo sapiens.
 XX WO2004050850-A2.
 PN 17-JUN-2004.
 PD 02-DEC-2003; 2003WO-US038234.
 PF 02-DEC-2002; 2002US-0430724P.
 PR (ABGE-) ARGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX WPI; 2004-461119/43.
 DR New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX Example 5; SEQ ID NO 215; 128pp; English.
 XX The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents the light chain from a monoclonal antibody
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.
 XX
 SQ Sequence 112 AA;
 Query Match 93.2%; Score 550; DB 8; Length 112;
 Best Local Similarity 93.8%; Pred. No. 8.7e-40;
 Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;
 QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
 Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
 QY 61 SGVPRFSGSGGTDFTLKISRVEADGVYYCMQALQSLMCSFGQGTGLEIK 113
 Db 61 SGVPRFSGSGGTDFTLKISRVEADGVYYCMQALQTI--TFGQGTGLEIK 111
 RESULT 15
 AEK98277
 ID AEK98277 standard; protein; 223 AA.
 XX AEK98277;
 AC AEK98277;
 XX 30-NOV-2006 (first entry)
 DT Human 161P2F10B antibody light chain SEQ ID NO 156.
 DE Cytostatic; 161P2F10B antagonist; Gene therapy; antibody production;
 KW cancer; neoplasm; therapeutic; light chain.
 XX Homo sapiens.
 OS WO2006105488-A2.
 PN 05-OCT-2006.
 PD 31-MAR-2006; 2006WO-US012314.
 PF 31-MAR-2005; 2005US-0667588P.
 XX

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PR 20-JUL-2005; 2005US-0700975P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Kanner SB, Challita-Eid PM, Perez-Villar JJ;
XX Satpaev D, Raitano AB, Morrison RK, Morrison KJM, Jia X, Gudas J;
XX WPI; 2006-680690/70.
XX
XX New monoclonal antibody that binds specifically to a 161P2F10B protein,
XX useful for treating prostate, pancreas, bladder, kidney, colon, lung,
XX ovary, or breast cancer.
XX
XX Disclosure; SEQ ID NO 156; 438pp; English.
XX
XX The invention relates to a monoclonal antibody or its antigen binding
XX fragment comprising an antigen binding site that binds specifically to a
XX 161P2F10B protein, where the monoclonal antibody is H16-7.213, H16-9.69,
XX H16-1.52, H16-1(1)23, H16-9.44, H16-1.67, H16-1(3,5)36, H16-1.86, H16-
XX 9.10, H16-9.33, H16-1.68, H16-1(1)11, H16-1(3,5)18, H16-1(2,4)4, H16-
XX -1(3,5)56, H16-1.93, H16-7.8, H16-1(3,5)27.1, H16-1.61, H16-1(3,5)5, H16-
XX -7.200, H16-1(3,5)42, H16-9.65, H16-1.29, H16-3.4, H16-1.92, H16-
XX 1(3,5)19, or H16-1.80. The monoclonal antibody or its fragment is useful
XX for preparing a medicament for the treatment of prostate, pancreas,
XX bladder, kidney, colon, lung, ovary, or breast cancer, where the
XX monoclonal antibody or its fragment is administered in combination with
XX radiation or a chemotherapeutic agent. The present sequence represents
XX the amino acid sequence of a human 161P2F10B antibody light chain.
XX
SQ Sequence 223 AA;
Query Match 93.2%; Score 550; DB 10; Length 223;
Best Local Similarity 93.8%; Pred. No. 1.8e-39;
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

OY 1 DIVMTQSPPLSLPVTGPEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRA 60
DB 8 DIVMTQSPPLSLPVTGPEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRA 67

OY 61 SGVPRFSGSGSGTDFTLKISRVEADDDGYYCMQALQSLMCSFGQGTKEIK 113
DB 68 SGVPRFSGSGSGTDFTLKISRVEADDDGYYCMQALQTI--TFGQGTREIK 118

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Search completed: April 25, 2007, 04:05:21
Job time : 98.9972 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:05:37 ; Search time 9 Seconds
(without alignments)
1261.509 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSLPLVPTGEPAS.....MQALQSLMCSFGQGTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545.5	92.5	132	2 S26882	Ig kappa chain V r
2	544.5	92.3	112	2 S58207	Ig light chain V r
3	544.5	92.3	135	2 S40342	Ig kappa chain - h
4	544.5	92.3	136	2 S40357	Ig kappa chain V-J
5	536.5	90.9	112	2 S58206	Ig light chain V r
6	535	90.7	126	2 S40339	Ig kappa chain - h
7	533.5	90.4	117	1 K2HUGM	Ig kappa chain pre
8	532.5	90.3	125	2 S40356	Ig kappa chain - h
9	508.5	86.2	113	1 K2HUTW	Ig kappa chain V-I
10	508.5	86.2	121	2 S40371	Ig kappa chain - h
11	508.5	86.2	131	2 S40372	Ig kappa chain V-J
12	505	85.6	123	2 S40319	Ig kappa chain V r
13	497	84.2	100	2 S24681	Ig kappa chain - h
14	487	82.5	114	2 S40375	Ig kappa chain - h
15	483.5	81.9	124	2 S03876	Ig kappa chain V-I
16	481	81.5	112	1 K2HUML	Ig kappa chain V-I
17	460	78.0	130	2 S40321	Ig kappa chain - h
18	456	77.3	115	1 K2HUCM	Ig kappa chain V-I
19	450.5	76.4	113	1 K2HUFH	Ig kappa chain V-I
20	447	75.8	87	2 S34091	Ig kappa chain V r
21	445	75.4	140	2 S22658	Ig kappa chain pre
22	442.5	75.0	112	2 F27887	Ig kappa chain V r
23	439.5	74.5	112	2 B27887	Ig kappa chain V r
24	439.5	74.5	113	2 PL0203	Ig kappa chain V r
25	439.5	74.5	126	2 S40312	anti-DNA autoantib
26	439.5	74.5	131	2 B39276	Ig kappa chain - h
27	439.5	74.5	131	2 D29380	Ig light chain pre
28	439	74.4	114	2 S49572	Ig kappa chain pre
29	439	74.4	130	2 C29380	Ig kappa chain pre

ALIGNMENTS

RESULT 1

S26882

Ig kappa chain V region (V607) - human
C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C;Accession: S26882

R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.

Nature 347, 90-92, 1990

A;Title: Megabase inversions in the human genome as physiological events.

A;Reference number: S26882; MUID:90370099; PMID:2118596

A;Accession: S26882

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-132 <WEI>

A;Cross-references: UNIPARC:UPI0000116D46; EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 92.5%; Score 545.5; DB 2; Length 132;
Best Local Similarity 93.8%; Pred. No. 1.2e-42; Mismatches 4; Indels 1; Gaps 1;
Matches 106; Conservative 2;

QY 1 DIVMTQSLPLVPTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLIYLGSNRA 60

DB 21 DIVMTQSLPLVPTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLIYLGSNRA 80

QY 61 SGVPDRPSGSGTGDTFTLKISRVEADVGVYVCMQALQSLMCSFGQGTKLEIK 113

DB 81 SGVPDRPSGSGTGDTFTLKISRVEADVGVYVCMQALQTPQ-TFGQGTKVEIK 132

RESULT 2

S58207

Ig light chain V region anti-F(ab')2 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000

C;Accession: S58207

R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,

submitted to the EMBL Data Library, July 1995

A;Description: Characterization of heavy and light chain immunoglobulin variable region

A;Reference number: S58206

A;Accession: S58207

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <WEL>

A;Cross-references: UNIPARC:UPI0000116253; EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 544.5; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.3e-42;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
DB 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

RESULT 3
S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40342
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; UNIPARC:UPI0000176CA7; EMBL:X72452; NID:g441372; PID:19-108/Domain: immunoglobulin homology <IMM>
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 92.3%; Score 544.5; DB 2; Length 135;
Best Local Similarity 93.8%; Pred. No. 1.5e-42;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 14 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 73
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
DB 74 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQTPR--TFGQGTKEIK 125

RESULT 4
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; UNIPARC:UPI0000176CA8; EMBL:X72467
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 92.3%; Score 544.5; DB 2; Length 136;
Best Local Similarity 93.8%; Pred. No. 1.5e-42;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 21 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 80

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
DB 81 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 132

RESULT 5
S58206
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58206
R:Welchot, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, R.;
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58206
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: UNIPARC:UPI0000116252; EMBL:X89054; NID:g929640; PIDN:CAA61441.1; PID:16-95/Domain: immunoglobulin homology <IMM>
C:Superfamily: immunoglobulin
C:Keywords: immunoglobulin

Query Match 90.9%; Score 536.5; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 6.7e-42;
Matches 104; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
DB 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQTPR--TFGQGTKEIK 112

RESULT 6
S40339
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40339
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40339
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <KLE>
A:Cross-references: UNIPARC:UPI0000116159; EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:16-95/Domain: immunoglobulin homology <IMM>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 90.7%; Score 535; DB 2; Length 126;
Best Local Similarity 92.0%; Pred. No. 1e-41;
Matches 104; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 16 DIVMTQSPSLPVTTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 75
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
DB 76 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQTPR--WTFGQGTKEIK 126

RESULT 7
K2HUGM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)


```
QY 64 PDRFSGSGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEIK 113
|||||
Db 61 PDRFSGSGTDTFTLKISRVEADVGYYCMQGLQT-PTTFQGTKEIK 109
|||||

RESULT 11
S40372
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40372
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40372
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: UNIPARC:UPI000011617A; EMBL:X72482; NID:9441432; PIDN:CAA51150.1; PID:19-548102.1; PDB:1YLG
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 508.5; DB 2; Length 131;
Best Local Similarity 88.4%; Pred. No. 2.7e-39;
Matches 99; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db 21 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSTRA 80
|||||

QY 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEI 112
|||||
Db 81 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQPLQT-PYTFQGTKEI 131
|||||

RESULT 12
S40319
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40319
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40319
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: UNIPARC:UPI0000116145; EMBL:X72429; NID:9441326; PIDN:CAA51097.1; PID:19-548102.1; PDB:1YLG
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-105/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 505; DB 2; Length 123;
Best Local Similarity 89.7%; Pred. No. 5.3e-39;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db 11 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 70
|||||

QY 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEI 107
|||||
Db 71 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQTPSVTSAGK 117
|||||

RESULT 13
S24681
Ig kappa chain - human
```

```
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S24681
R:van Es, J.H.
submitted to the EMBL Data Library, July 1992
A:Reference number: S24679
A:Accession: S24681
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <VAN>
A:Cross-references: UNIPARC:UPI00001160E1; EMBL:X67904; NID:933435; PIDN:CAA48102.1; PID:19-548102.1; PDB:1YLG
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 497; DB 2; Length 100;
Best Local Similarity 96.0%; Pred. No. 2.3e-38;
Matches 95; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||

QY 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEI 99
|||||
Db 61 SGVPRFSGSGTDTFTLKISRVEADVGYYCMQALQT 99
|||||

RESULT 14
S40375
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40375
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40375
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-114 <KLE>
A:Cross-references: UNIPARC:UPI000011617D; EMBL:X72485; NID:9441438; PIDN:CAA51153.1; PID:19-548102.1; PDB:1YLG
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 487; DB 2; Length 114;
Best Local Similarity 89.4%; Pred. No. 2.1e-37;
Matches 93; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRAGV 63
|||||
Db 1 MTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRAGV 60
|||||

QY 64 PDRFSGSGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTKEI 107
|||||
Db 61 PDRFSGSGTDTFTLKISRVEADVGYYCMQALQTSVTSAGK 104
|||||

RESULT 15
S03876
Ig kappa chain V-II region (Inc) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S03876
R:Perri, G.; Stoppani, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989
A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
A:Reference number: S03876; MUID:89194238; PMID:2495028
A:Accession: S03876
A:Molecule type: protein
A:Residues: 1-124 <PER>
```

A;Cross-references: UNIPARC:UPI000017679D
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
Query Match 81.9%; Score 483.5; DB 2; Length 124;
Best Local Similarity 83.2%; Pred. No. 4.8e-37;
Matches 94; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
Qy 1 DIVVTOSPLSLPVTGPEPASISCKSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLGSNRA 60
Db 1 DIVVTOSPLSLPVTGPEPASISCKSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLGSNRA 60
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDFTSGSGGTDFTLLISVVGAEDVGYYVYCMQALQT-PWTFGGQTKVGIK 112

Search completed: April 25, 2007, 04:06:40
Job time : 9.61864 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 03:58:23 ; Search time 77 Seconds
(without alignments)
1574.822 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSPLEVTPEPAS.....MOALQSLMGCSFGQGTLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	533.5	90.4	117	1	KV2E_HUMAN	P06309 homo sapien
2	532.5	90.3	239	2	ORNEKO_HUMAN	Q8NEK0 homo sapien
3	532	90.2	240	2	Q6FIH6_HUMAN	Q6FIH6 homo sapien
4	508.5	86.2	113	1	KV2D_HUMAN	P01617 homo sapien
5	481	81.5	112	1	KV2C_HUMAN	P01616 homo sapien
6	456	77.3	115	1	KV2A_HUMAN	P01614 homo sapien
7	450.5	76.4	113	1	KV2B_HUMAN	P01615 homo sapien
8	436.5	74.0	133	1	KV2F_HUMAN	P06310 homo sapien
9	436.5	74.0	248	2	Q6SZQ7_MOUSE	Q6SZQ7 mus sp. b3(
10	436	73.9	115	2	Q5F2I0_MOUSE	Q5F2I0 mus musculus
11	429.5	72.8	239	2	Q8TCD0_HUMAN	Q8TCD0 homo sapien
12	429.5	72.8	239	2	Q58EU8_MOUSE	Q58EU8 mus musculus
13	428.5	72.6	239	2	Q6P491_HUMAN	Q6P491 homo sapien
14	427	72.4	114	2	Q9UL80_HUMAN	Q9UL80 homo sapien
15	426.5	72.3	113	1	KV2G_MOUSE	P01631 mus musculus
16	418.5	70.9	219	2	Q6SZC0_MOUSE	Q6SZC0 mus musculus
17	416.5	70.6	113	1	KV2E_MOUSE	P03976 mus musculus
18	415.5	70.4	112	2	Q53VP8_MOUSE	Q53VP8 mus musculus
19	413.5	70.1	234	2	Q5XKG4_MOUSE	Q5XKG4 mus musculus
20	407.5	69.1	113	1	KV2F_MOUSE	P01630 mus musculus
21	406.5	68.9	112	1	KV2D_MOUSE	P01629 mus musculus
22	396.5	67.2	112	2	Q6LEM8_MOUSE	Q6LEM8 mus musculus
23	388.5	65.8	113	1	KV2C_MOUSE	P01628 mus musculus
24	388	65.8	108	1	KV1_CANFA	P01618 canis fami
25	386.5	65.5	112	1	KV2A_MOUSE	P01626 mus musculus
26	380	64.4	114	1	KV4A_HUMAN	P01625 homo sapien
27	373	63.2	120	1	KV2B_MOUSE	P01627 mus musculus
28	372	63.1	134	1	KV4C_HUMAN	P06314 homo sapien
29	365.5	61.9	133	1	KV4B_HUMAN	P06313 homo sapien
30	361	61.2	255	2	Q6KB05_MOUSE	Q6KB05 mus musculus
31	355.5	60.3	109	1	KV3E_HUMAN	P01623 homo sapien

32	354	60.0	240	2	Q52L64_MOUSE	Q52L64 mus musculus
33	352.5	59.7	109	1	KV3B_HUMAN	P01620 homo sapien
34	352.5	59.7	109	1	KV3D_HUMAN	P01622 homo sapien
35	349	59.2	236	2	Q6PIL8_HUMAN	Q6PIL8 homo sapien
36	348.5	59.1	129	1	KV3L_HUMAN	P18135 homo sapien
37	347.5	58.9	129	1	KV3M_HUMAN	P18136 homo sapien
38	345.5	58.6	109	2	Q9UL78_HUMAN	Q9UL78 homo sapien
39	345	58.5	111	1	KV3S_MOUSE	P01671 mus musculus
40	345	58.5	111	2	Q920E9_MOUSE	Q920E9 mus musculus
41	344	58.3	111	1	KV3R_MOUSE	P01670 mus musculus
42	344	58.3	111	1	KV3U_MOUSE	P01673 mus musculus
43	342.5	58.1	109	1	KV3G_HUMAN	P04206 homo sapien
44	340.5	57.7	235	2	Q6GMW0_HUMAN	Q6GMW0 homo sapien
45	338.5	57.4	108	1	KV3A_HUMAN	P01619 homo sapien

ALIGNMENTS

RESULT 1

ID	KV2E_HUMAN	STANDARD;	PRT;	117 AA.
AC	P06309;			
DT	01-JAN-1988, integrated into UniProtKB/Swiss-Prot.			
DT	01-JAN-1988, sequence version 1.			
DT	27-JUN-2006, entry version 47.			
DE	Ig kappa chain V-II region GM607 precursor (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;			
OC	Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
RX	MEDLINE:84191506; PubMed:6325927; DOI=10.1038/309073a0;			
RA	Klobeck H.G., Solomon A., Zachau H.G.;			
RT	"Contribution of human V kappa II germ-line genes to light-chain			
RT	diversity."			
RL	Nature 309:73-76(1984).			
CC				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC				
CC	EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.			
DR	PIR; A01889; K2HUGM.			
DR	HSSP; Q99M37; 1191.			
DR	SWR; P06309; 5-115.			
DR	LinkHub; P06309; -.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003599; Ig_sub.			
DR	InterPro; IPR013106; Ig_V-set.			
DR	InterPro; IPR003596; Ig_V-set_sub.			
DR	Fram; PF07686; V-set; 1.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00406; IG; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.			
FT	SIGNAL	<1	4	
FT	CHAIN	5	117	
FT	REGION	5	27	
FT	REGION	28	43	
FT	REGION	44	58	
FT	REGION	59	65	
FT	REGION	66	96	
FT	REGION	98	106	
FT	REGION	107	116	
FT	DISULFID	27	97	
FT	NON_TER	1	1	
FT	NON_TER	117	117	

Ig kappa chain V-II region GM607.
/FTID:PRO_0000015172.
Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.


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SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
Query Match 90.4%; Score 533.5; DB 1; Length 117;
Best Local Similarity 92.0%; Pred. No. 2,7e-49;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHGNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHGNYLDWYLOKPGQSPQLLIYLGSNRA 64
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQALQSLMCSFGQGTKEIK 113
|||||
Db 65 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQALQSLMCSFGQGTKEIK 116
|||||

RESULT 2
Q8NEKO HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 27-JUN-2006, entry version 30.
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92289816; PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565 (1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation."
RL Eur. J. Immunol. 23:391-397 (1993).
```

```
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94080891; PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation."
RL Eur. J. Immunol. 23:3248-3262 (1993).
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
CC
EMBL: BC030814; AAH30814.1; -; mRNA.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 1172.
DR SMR; Q8NEKO; 21-237.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1-set.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003599; IG_sub.
DR InterPro; IPR013106; IG_V-set.
DR InterPro; IPR003596; IG_V-set_sub.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Immunoglobulin domain; Membrane; Repeat; Transmembrane.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 90.3%; Score 532.5; DB 2; Length 239;
Best Local Similarity 90.3%; Pred. No. 8.5e-49;
Matches 102; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHGNYLDWYLOKPGQSPQLLIYLGSNRA 60
|||||
Db 21 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHGNYLDWYLOKPGQSPQLLIYLGSNRA 80
|||||

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQALQSLMCSFGQGTKEIK 113
|||||
Db 81 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQALQSLMCSFGQGTKEIK 132
|||||

RESULT 3
Q6PIH6 HUMAN PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 27-JUN-2006, entry version 21.
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92289816; PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
V kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565 (1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation."
RL Eur. J. Immunol. 23:391-397 (1993).
```



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RESULT 5
KV2C_HUMAN
ID   KV2C_HUMAN          STANDARD;          PRT;          112 AA.
AC   P01616;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   21-JUL-1986, sequence version 1.
DT   30-MAY-2006, entry version 41.
DE   Ig kappa chain V-II region MIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=68242259; PubMed=5586923;
RA   Hilschmann N.;
RT   "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT   type).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722 (1967).
RN   [2]
RP   SEQUENCE REVISION TO 50; 52; 96 AND 97.
RX   MEDLINE=70063440; PubMed=4188189;
RA   Hilschmann N.;
RT   "Molecular basis of antibody formation.";
RL   Naturwissenschaften 56:195-205 (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR   PIR; B91639; K2HUCM.
DR   HSSP; P01751; INQB.
DR   SMR; P01614; 2-115.
DR   LinkHub; P01614; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig-sub.
DR   InterPro; IPR013106; Ig_V-set.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   CHAIN          1  >112
FT   REGION         1  23
FT   REGION         24  38
FT   REGION         39  53
FT   REGION         54  60
FT   REGION         61  92
FT   REGION         93  101
FT   REGION         102  111
FT   REGION         123  92
FT   DISULFID       23  92
FT   NON_TER       112  112
SQ   SEQUENCE      112 AA; 12057 MW; E5B22E2FA7ABE481 CRC64;

Query Match          81.5%; Score 481; DB 1; Length 112;
Best Local Similarity 80.5%; Pred. No. 1-2e-43;
Matches 91; Conservative 16; Mismatches 4; Indels 2; Gaps 2;

QY   1  DIVMTQSPISLPTVTPGPASISCRSSQSLHSGNYLDWYLQKPGQSPOLLIVLGSNRA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   1  DIVLTQSPISLPTVTPGPASISCRSSQSLHSGNYLDWYLKPGZSPZLLIVLGSNRA 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY   61  SGVPRFSGSGGTFTLKISRVEADDDVGYVCMQALQSLMCSFGQGTKEIK 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   60  SGVPRFSGSGGTFTLKISRVAZBVGYYVCMQALQTPLE-TFGGGTIVEIK 111
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2A_HUMAN
ID   KV2A_HUMAN          STANDARD;          PRT;          115 AA.
AC   P01614;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   21-JUL-1986, sequence version 1.
DT   30-MAY-2006, entry version 45.
DE   Ig kappa chain V-II region Cum.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=68242259; PubMed=5586923;
RA   Hilschmann N.;
RT   "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT   type).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722 (1967).
RN   [2]
RP   SEQUENCE REVISION TO 50; 52; 96 AND 97.
RX   MEDLINE=70063440; PubMed=4188189;
RA   Hilschmann N.;
RT   "Molecular basis of antibody formation.";
RL   Naturwissenschaften 56:195-205 (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR   PIR; B91639; K2HUCM.
DR   HSSP; P01751; INQB.
DR   SMR; P01614; 2-115.
DR   LinkHub; P01614; -.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig-sub.
DR   InterPro; IPR013106; Ig_V-set.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   CHAIN          1  >112
FT   REGION         1  23
FT   REGION         24  38
FT   REGION         39  53
FT   REGION         54  60
FT   REGION         61  92
FT   REGION         93  101
FT   REGION         102  111
FT   REGION         123  92
FT   DISULFID       23  92
FT   NON_TER       112  112
SQ   SEQUENCE      112 AA; 12057 MW; E5B22E2FA7ABE481 CRC64;

Query Match          77.3%; Score 456; DB 1; Length 115;
Best Local Similarity 81.6%; Pred. No. 6.2e-41;
Matches 93; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

QY   1  DIVMTQSPISLPTVTPGPASISCRSSQSLHSGNYLDWYLQKPGQSPOLLIVLGSNR 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   2  DIVMTQTPISLPTVTPGPASISCRSSQSLDSDGNTYLNWYLQKAGQSPOLLIVLTSYR 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY   60  ASGVPRFSGSGGTFTLKISRVEADDDVGYVCMQALQSLMCSFGQGTKEIK 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   62  ASGVPRFSGSGGTFTLKISRVAQEDVDGVGYVCMQRL-IPYTFGGGTKEIR 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
KV2B_HUMAN
ID   KV2B_HUMAN          STANDARD;          PRT;          113 AA.
AC   P01615;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   21-JUL-1986, sequence version 1.
DT   30-MAY-2006, entry version 43.
DE   Ig kappa chain V-II region FR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
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RN  PROTEIN SEQUENCE.
RX  MEDLINE=76253627; PubMed=821524;
RA  Riesen W.F., Jaton J.-C.;
RT  "Variable region sequence of the light chain from a Waldenstroms IgM
RL  with specificity for phosphorylcholine.";
RL  Biochemistry 15:3829-3833(1976).
CC  -I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC  macroglobulin that binds phosphorylcholine.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  PIR; A01886; K2HURF.
DR  HSSP; Q99M37; 1191.
DR  SMR; P01615; 1-109.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003599; Ig sub.
DR  InterPro; IPR013106; Ig V-set.
DR  InterPro; IPR003596; Ig_V-set_sub.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IGV; 1.
DR  PROSITE; PS00835; IG_LIKE; 1.
KW  Direct protein sequencing; Immunoglobulin domain;
KW  Immunoglobulin V region.
FT  CHAIN 1 >113
FT  Ig kappa chain V-II region FR.
FT  /FTID=PRO_0000059759.
FT  Framework-1.
FT  REGION 1 23 Complementarity-determining-1.
FT  REGION 24 39 Complementarity-determining-1.
FT  REGION 40 54 Complementarity-determining-2.
FT  REGION 55 61 Complementarity-determining-2.
FT  REGION 62 93 Complementarity-determining-3.
FT  REGION 94 102 Complementarity-determining-3.
FT  REGION 103 112 Complementarity-determining-3.
FT  REGION 112 112 By similarity.
FT  DISULFID 23 93
FT  NON_TER 113 113
SQ  SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 76.4%; Score 450.5; DB 1; Length 113;
Best Local Similarity 77.0%; Pred. No. 2.4e-40;
Matches 87; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIWMTQSPFLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
Db 1 DVVMTQSPFLPVTGPEPASISCRSSQSLVRYRGTYLWYLQKPGQSPQLLIYLGSSYRD 60

QY 61 SGVPRFSGSGGTFTLKISRVEADPGVYVCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPRFSGSGGTFTLKISRVEADPGVYVCMQATZS-PYTFGGGTKEIK 112

RESULT 8
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DT 30-MAY-2006, entry version 43.
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combrliato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
```

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III.";
Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR  EMBL; Z00020; CAA77315.1; -; Genomic_DNA.
DR  PIR; A01890; K2HURF.
DR  HSSP; Q99M37; 1191.
DR  SMR; P06310; 21-133.
DR  Ensembl; ENSG00000173758; Homo sapiens.
DR  LinkHub; P06310; -.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003599; Ig sub.
DR  InterPro; IPR013106; Ig_V-set.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IGV; 1.
DR  PROSITE; PS00835; IG_LIKE; 1.
KW  Immunoglobulin domain; Immunoglobulin V region; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 133
FT  Ig kappa chain V-II region RPMI 6410.
FT  /FTID=PRO_0000015173.
FT  Framework-1.
FT  REGION 21 43 Complementarity-determining-1.
FT  REGION 44 59 Complementarity-determining-2.
FT  REGION 60 74 Complementarity-determining-2.
FT  REGION 75 81 Complementarity-determining-3.
FT  REGION 82 113 Complementarity-determining-3.
FT  REGION 114 122 Complementarity-determining-3.
FT  REGION 123 132 Complementarity-determining-3.
FT  DISULFID 43 113 By similarity.
FT  NON_TER 133 133
SQ  SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 74.0%; Score 436.5; DB 1; Length 133;
Best Local Similarity 76.1%; Pred. No. 9.4e-39;
Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIWMTQSPFLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
Db 21 DVVMTQSPFLPVTGPEPASISCRSSQSLVRYRGTYLWYLQKPGQSPQLLIYKVSNRD 80

QY 61 SGVPRFSGSGGTFTLKISRVEADPGVYVCMQALQSLMCSFGQGTKEIK 113
Db 81 SGVPRFSGSGGTFTLKISRVEADPGVYVCMQGTGTH-WSWTFGGGTKEIK 132

RESULT 9
Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 18-APR-2006, entry version 11.
DE B3(Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
CC -----
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RESULT 13
Q6P491 HUMAN PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 27-JUN-2006, entry version 22.
DE Hypothetical protein LOC651928.
GN Name=LOC651928;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC063599; AAH63599.1; -; mRNA.
CC HSSP; P01837; 1KCU.
CC SMR; O6P491; 21-237.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0006020; C:membrane; IEA.
CC GO; GO:0030106; F:MHC class I receptor activity; IEA.
CC GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
CC GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_C1-set.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003599; Ig_sub.
CC InterPro; IPR013106; Ig_V-set.
CC InterPro; IPR003596; Ig_V-set_sub.
CC Pfam; PF07654; C1-set; 1.
CC Pfam; PF07686; V-set; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00407; IGc1; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
CC PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain; Membrane; Repeat;
KW Transmembrane.
SQ SEQUENCE 239 AA; 26246 MW; CD7313DDFFD358B3 CRC64;
Query Match 72.6%; Score 428.5; DB 2; Length 239;
Best Local Similarity 75.2%; Pred. No. 1.4e-37;
Matches 85; Conservative 11; Mismatches 16; Indels 1; Gaps 1;
QY 1 DIVMTQSLPLSPVTPGEPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYLGSNRA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 DIVMTQTPLSPPVTLGQPASISCRSSQSLHNSNGYNLDWYLQKPGQSPQLLIYKISNRF 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSGSTDTFLTKISRVEADGVVYCMQALQSLMCSFGQGTKEIK 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGVPDRFSGSGAGTDTFLTKISRVEADGVVYCMQ-VSHFPRTRGQGTTRVEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 14
Q9UL80 HUMAN PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 18-APR-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92352481; PubMed=1322670;
RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA Gaskin F., Fu S.M.;
RT "A rheumatoid factor from a normal individual encoded by VH2 and V
kappa II gene segments."
RL Arthritis Rheum. 35:900-904 (1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the v kappa locus and do not show
somatic mutation."
RL Eur. J. Immunol. 23:391-397 (1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92289816; PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing v kappa-J kappa recombination after formation of a productive
v kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565 (1992).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AF035034; AAD56270.1; -; mRNA.
CC PIR; B49002; B49002.
CC PIR; S23638; S23638.
CC PIR; S34094; S34094.
CC PIR; S34095; S34095.
CC HSSP; P01625; ILVE.
CC SMR; Q9UL80; 1-114.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig_sub.
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DR InterPro; IPR013106; Ig_V-set.
DR InterPro; IPR003596; Ig_V-set_sub.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070B31E210D1CB01 CRC64;

Query Match 72.4%; Score 427; DB 2; Length 114;
Best Local Similarity 74.3%; Pred. No. 8.2e-38;
Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNLDWYLQKPGQSPOLLIVLGSNRA 60
Db 1 DVMTQSPSLPVTLRQPAISICRSCSPVSYDGNLYLNWFQORPGQSPRLIKVSNRD 60

QY 61 SGVDPFRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKLEIK 113
Db 61 SGVDPFRFSGSGGTDTFTLKISRVEADVGYYVCMQGTHTWPPWTFGGQTKVEIK 113

Search completed: April 25, 2007, 04:06:36
Job time : 77.9294 secs

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RESULT 15
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ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 30-MAY-2006, entry version 40.
DE IG kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
protein that binds digoxin.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC PIR; A01914; KVM526.
DR HSSP; Q99M37; I191.
DR Ensembl; ENSMUSG0000005315; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR InterPro; IPR013106; Ig_V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT FT 1 >113
FT CHAIN 1 >113
FT REGION 1 23
FT REGION 24 39
FT REGION 40 54
FT REGION 55 61
FT REGION 62 93
FT REGION 94 102
FT REGION 103 112
FT Framework-1.
FT Framework-2.
FT Framework-3.
FT Framework-4.

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FT DISULFID 23 93 By similarity.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 72.3%; Score 426.5; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 9.2e-38;
Matches 84; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNLDWYLQKPGQSPOLLIVLGSNRA 60
Db 1 DVMTQSPSLPVTSLGDAQASISCRSSQSLVHSHNGNTLYLNWYLQKAGQSPKLLIKVSNRF 60

QY 61 SGVDPFRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKLEIK 113
Db 61 SGVDPFRFSGSGGTDTFTLKISRVEADVGYYVCMQGTHTWPPWTFGGQTKLEIK 113

Search completed: April 25, 2007, 04:06:36
Job time : 77.9294 secs

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:06:51 ; Search time 14 Seconds
(without alignments)
696.311 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIWMTQSPSLPVTPEPAS.....MOALQSLMCSFGQTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6 COMB.pcp:*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7 COMB.pcp:*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/8 COMB.pcp:*
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- 6: /EMC_Celerra_SID33/ptodata/2/iaa/10 COMB.pcp:*
- 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547.5	92.8	113	2	US-09-025-769B-15: Sequence 15, Appl
2	547.5	92.8	113	2	US-09-490-070A-15: Sequence 15, Appl
3	547.5	92.8	113	2	US-09-490-153-15: Sequence 15, Appl
4	547.5	92.8	113	2	US-09-490-324-15: Sequence 15, Appl
5	544.5	92.3	112	2	US-09-254-180C-9: Sequence 9, Appl
6	533.5	90.4	112	1	US-08-331-398A-49: Sequence 49, Appl
7	533.5	90.4	112	1	US-08-331-397B-49: Sequence 49, Appl
8	533.5	90.4	112	1	US-08-759-804A-49: Sequence 49, Appl
9	533.5	90.4	112	2	US-09-227-693-49: Sequence 49, Appl
10	530.5	89.9	112	2	US-10-330-613A-2: Sequence 2, Appl
11	521.5	88.4	114	2	US-09-025-769B-29: Sequence 29, Appl
12	521.5	88.4	114	2	US-09-025-769B-45: Sequence 45, Appl
13	521.5	88.4	114	2	US-09-490-070A-29: Sequence 29, Appl
14	521.5	88.4	114	2	US-09-490-070A-45: Sequence 45, Appl
15	521.5	88.4	114	2	US-09-490-153-29: Sequence 29, Appl
16	521.5	88.4	114	2	US-09-490-153-45: Sequence 45, Appl
17	521.5	88.4	114	2	US-09-490-324-29: Sequence 29, Appl
18	521.5	88.4	114	2	US-09-490-324-45: Sequence 45, Appl
19	521.5	88.4	281	2	US-09-025-769B-178: Sequence 178, App
20	521.5	88.4	281	2	US-09-490-070A-178: Sequence 178, App
21	521.5	88.4	281	2	US-09-490-153-178: Sequence 178, App
22	521.5	88.4	281	2	US-09-490-324-178: Sequence 178, App
23	520.5	88.2	113	1	US-08-082-623-4: Sequence 4, Appl
24	519.5	88.1	112	1	US-10-330-613A-38: Sequence 38, Appl
25	512.5	86.9	112	1	US-08-053-171-16: Sequence 16, Appl
26	510	86.4	100	2	US-09-472-087-115: Sequence 115, App

27	510	86.4	100	2	US-10-194-975-79: Sequence 79, Appl
28	510	86.4	100	2	US-10-194-975-80: Sequence 80, Appl
29	510	86.4	100	2	US-10-330-613A-71: Sequence 71, Appl
30	505.5	85.7	112	2	US-09-000-088-2: Sequence 2, Appl
31	502.5	85.2	112	2	US-09-240-274-30: Sequence 30, Appl
32	502.5	85.2	112	2	US-09-848-798-30: Sequence 30, Appl
33	499.5	84.7	112	1	US-08-478-039-88: Sequence 88, Appl
34	499.5	84.7	112	1	US-08-476-349A-88: Sequence 88, Appl
35	499.5	84.7	239	2	US-10-000-489-8: Sequence 8, Appl
36	499.5	84.7	239	2	US-09-992-095B-8: Sequence 8, Appl
37	499.5	84.7	239	3	US-10-000-986A-8: Sequence 8, Appl
38	494.5	83.8	108	1	US-08-488-113B-151: Sequence 151, App
39	494.5	83.8	108	1	US-08-477-669D-15: Sequence 15, App
40	494.5	83.8	108	1	US-08-107-669D-15: Sequence 15, App
41	494.5	83.8	108	1	US-08-477-788A-15: Sequence 15, App
42	494.5	83.8	108	1	US-08-477-531B-15: Sequence 15, App
43	494.5	83.8	108	1	US-08-646-360-151: Sequence 151, App
44	494.5	83.8	108	1	US-08-082-842A-15: Sequence 15, App
45	494.5	83.8	108	2	US-08-839-765-151: Sequence 151, App

ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 630064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthum, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/025,769B
; APPLICATION NUMBER: 18-FEB-1998
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-15
Query Match 92.8%; Score 547.5; DB 2; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
 Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
 QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQI-PYTFGGGKLEIK 113
 Db 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQI-PYTFGGGKLEIK 112

RESULT 2

US-09-490-070A-15
 ; Sequence 15, Application US/09490070A
 ; Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Peter

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-070A-15

Query Match 92.8%; Score 547.5; DB 2; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60

Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQI-PYTFGGGKLEIK 113

Db 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQI-PYTFGGGKLEIK 112

RESULT 3

US-09-490-153-15

; Sequence 15, Application US/09490153

; Patent No. 6706484

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Peter

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-153-15

Query Match 92.8%; Score 547.5; DB 2; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQI-PYTFGGGKLEIK 113

Db 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQI-PYTFGGGKLEIK 112

RESULT 4

US-09-490-324-15

; Sequence 15, Application US/09490324

; Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ilag, Peter

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 113 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-490-153-15

Query Match 92.8%; Score 547.5; DB 2; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.3e-46;

Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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; FILING DATE: 24-Jan-2000
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-324-15
Query Match 92.8%; Score 547.5; DB 2; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.3e-46;
Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Db 1 DIVVTQSPLSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLSNRA 60
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Db 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQTPYTFGGQTKLEIK 112

RESULT 5
US-09-254-180C-9
; Sequence 9, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, KO
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
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; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-9
Query Match 92.3%; Score 544.5; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.6e-46;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

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Db 1 DIVVTQSPLSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLSNRA 60
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Db 61 SGVPRFSGSGGTDFTLKISRVEADVGYYVCMQALQTPYTFGGQTKLEIK 112

RESULT 6
US-08-331-398A-49
; Sequence 49, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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/ NAME/KEY: Protein
/ LOCATION: 1..112
/ OTHER INFORMATION: /note="Human IgM antibody GM607
/ OTHER INFORMATION: Variable Light Chain (V-L)"
US-08-331-397B-49

Query Match          90.4%; Score 533.5; DB 1; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.1e-45;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTLTKISRVAEADVGVYCMQALQSLMCSFGQGTKEIK 113
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RESULT 7
US-08-331-397B-49
; Sequence 49, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note="Human IgM antibody GM607
; OTHER INFORMATION: Variable Light Chain (V-L)"
US-08-331-397B-49
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Query Match          90.4%; Score 533.5; DB 1; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.1e-45;
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QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSHNGNYLDWYLOKPGQSPQLLIYLGSNRA 60
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Db 61 SGVPRFSGSGGTDTLTKISRVAEADVGVYCMQALQSLMCSFGQGTKEIK 112

RESULT 8
US-08-759-804A-49
; Sequence 49, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; SOFTWARE: Patent In Release #1.0, Version #1.30
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; FILING DATE: 03-DEC-1996
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; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note="Human IgM antibody GM607
; OTHER INFORMATION: Variable Light Chain (V-L)"
US-08-759-804A-49
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Query Match 90.4%; Score 533.5; DB 1; Length 112;

Best Local Similarity 92.0%; Pred. No. 3.1e-45;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
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Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

RESULT 9
US-09-227-693-49
; Sequence 49, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note="Human IgM GM607 VL region"
US-09-227-693-49

Query Match 90.4%; Score 533.5; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.1e-45;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60
Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

RESULT 10
US-10-330-613A-2
; Sequence 2, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-2

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Best Local Similarity 92.0%; Pred. No. 6.2e-45;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60
Db 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGQSPOLLIIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYVCMQALQSLMCSFGQGTKEIK 112

RESULT 11
US-09-025-769B-29
; Sequence 29, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 114 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-025-769B-29

Query Match      88.4%; Score 521.5; DB 2; Length 114;
Best Local Similarity 90.3%; Pred. No. 4.8e-44;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTPEGPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
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QY 61 SGVPDRFSGSGGTDTFTLKISRVEADGVVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADGVVYCMQALQSLMCSFGQGTKEIK 112

RESULT 13
US-09-490-070A-29
/ Sequence 29, Application US/09490070A
/ Patent No. 6696248
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
/ STREET: 1666 K Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20006
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/490,070A
/ FILING DATE: 24-Jan-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Colin G. Sandercock, Esq.
/ REGISTRATION NUMBER: 31,298
/ REFERENCE/DOCKET NUMBER: 37629-0005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 912-2000
/ TELEFAX: (202) 912-2020
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 114 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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US-09-490-070A-29

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Best Local Similarity 90.3%; Pred. No. 4.8e-44;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

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QY 61 SGVPDRFSGSGGTDTFTLKISRVEADGVVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADGVVYCMQALQSLMCSFGQGTKEIK 112

RESULT 12
US-09-025-769B-45
/ Sequence 45, Application US/09025769B
/ Patent No. 630064
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Plueckthun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 114 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein

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Ge, Liming
  Monney, Simon
  Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
  STREET: 1251 Avenue of the Americas
  CITY: New York
  STATE: New York
  COUNTRY: USA
  ZIP: 10021
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/490,153
  FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/025,769B
  FILING DATE: 18-FEB-1998
  APPLICATION NUMBER: EP 95 11 3021.0
  FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
  NAME: James F. Haley, Jr., Esq.
  REGISTRATION NUMBER: 27,794
  REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212)596-9000
  TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 29:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 114 amino acids
    TYPE: amino acid
    STRANDEDNESS: <Unknown>
    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-153-29

Query Match      88.4%; Score 521.5; DB 2; Length 114;
Best Local Similarity 90.3%; Pred. No. 4.8e-44;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DIWVTQSPSLPVTTPGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRA 60
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Qy 61 SGVPDRFSGSGGTDFTLKISRVEADVGYYCWAQLQSLWCSFGQGTKEIK 113
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Job time : 15.2048 secs

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: April 25, 2007, 04:18:18 ; Search time 42 Seconds
(without alignments)
1251.741 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

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Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	590	100.0	113	4	US-10-041-860-30	Sequence 30, Appl
2	590	100.0	113	4	US-10-041-860-221	Sequence 221, App
3	590	100.0	113	4	US-10-041-860-255	Sequence 255, App
4	590	100.0	113	4	US-10-665-383-40	Sequence 40, Appl
5	576.5	97.7	114	4	US-10-041-860-322	Sequence 322, App
6	554	93.9	113	6	US-11-021-715-89	Sequence 89, Appl
7	550	93.2	112	5	US-10-726-332-215	Sequence 215, App
8	549	93.1	113	6	US-11-021-715-88	Sequence 88, Appl
9	548.5	93.0	110	4	US-10-309-762-165	Sequence 165, App
10	548.5	93.0	112	6	US-11-021-715-74	Sequence 74, Appl
11	547.5	92.8	112	4	US-10-292-088-104	Sequence 104, App
12	547.5	92.8	112	6	US-11-021-715-75	Sequence 75, Appl
13	547.5	92.8	112	6	US-11-021-715-92	Sequence 92, Appl
14	547.5	92.8	113	5	US-10-834-397-15	Sequence 15, Appl
15	547	92.7	112	5	US-10-726-332-24	Sequence 24, Appl
16	546.5	92.6	112	6	US-11-021-715-77	Sequence 77, Appl
17	546.5	92.6	134	5	US-10-858-855-8	Sequence 8, Appl
18	546	92.5	111	5	US-10-727-155-276	Sequence 276, App
19	546	92.5	112	5	US-10-725-962-42	Sequence 42, Appl
20	545.5	92.5	112	5	US-10-735-916A-58	Sequence 58, Appl
21	545.5	92.5	112	6	US-11-012-353-58	Sequence 58, Appl
22	545.5	92.5	113	4	US-10-308-817-177	Sequence 177, App
23	545.5	92.5	113	4	US-10-453-698-177	Sequence 177, App
24	544.5	92.3	112	4	US-10-292-088-103	Sequence 103, App
25	544.5	92.3	112	4	US-10-292-088-111	Sequence 111, App
26	544.5	92.3	112	5	US-10-877-773-30	Sequence 30, Appl
27	544.5	92.3	112	5	US-10-877-774-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-10-041-860-30

; Sequence 30, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadl

; APPLICANT: Weber, Richard

; APPLICANT: Bezabeh, Binyam

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ABGENIX.051A

; CURRENT APPLICATION NUMBER: US/10/041,860

; CURRENT FILING DATE: 2002-01-07

; NUMBER OF SEQ ID NOS: 377

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 113

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-041-860-30

Query Match 100.0%; Score 590; DB 4; Length 113;

Best Local Similarity 100.0%; Pred. No. 4.3e-46;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNYLDWYKPKGSPQLLIYLSNRA 60

DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSGNYLDWYKPKGSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSGGTDTFTLKISRVEADDDVGVYYCMQALQSLMCSFGQGTGLEIK 113

DB 61 SGVPDRFSGSGGTDTFTLKISRVEADDDVGVYYCMQALQSLMCSFGQGTGLEIK 113

RESULT 2

US-10-041-860-221

; Sequence 221, Application US/10041860

; Publication No. US20030157109A1

; GENERAL INFORMATION:

; APPLICANT: Corvalan, Jose R.F.

; APPLICANT: Jia, Xiao-Chi

; APPLICANT: Feng, Xiao

; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine

; APPLICANT: Gazit, Gadl


```
; Sequence 89, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-89

Query Match          93.9%; Score 554; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 8.2e-43;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113

RESULT 7
US-10-726-332-215
; Sequence 215, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-215

Query Match          93.2%; Score 550; DB 5; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.9e-42;
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113

; Sequence 89, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-89

Query Match          93.9%; Score 554; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 8.2e-43;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113

RESULT 7
US-10-726-332-215
; Sequence 215, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-215

Query Match          93.2%; Score 550; DB 5; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.9e-42;
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113

; Sequence 89, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-89

Query Match          93.1%; Score 549; DB 6; Length 113;
Best Local Similarity 92.9%; Pred. No. 2.4e-42;
Matches 105; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
QY 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113
Db 61 SGVPDRFSGSGGTDTFTLKISRVEADVGYYCMQALQSLMCSFGQGTGLEIK 113

RESULT 9
US-10-309-762-165
; Sequence 165, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-165

Query Match          93.0%; Score 548.5; DB 4; Length 110;
Best Local Similarity 94.7%; Pred. No. 2.5e-42;
Matches 107; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
Db 1 DIVMTQSLPLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLSNRA 60
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Qy 61 SGVPDRFSGSGGTDFTLKISRVEADDDGVVYCMQALQSLMCSFGQTKLEIK 113
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 Db 61 SGVPDRFSGSGGTDFTLKISRVEADDDGVVYCMQALQSLMCSFGQTKLEIK 110
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RESULT 10
US-11-021-715-74
; Sequence 74, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-74

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[illegible]

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RESULT 11
US-10-292-088-104
; Sequence 104, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-104

```

Query Match 92.8%; Score 547.5; DB 4; Length 112;
Best Local Similarity 94.7%; Pred. No. 3.2e-42;
Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
OV 1 DIWVTSPISLPVTGPEPASICRSSOSLIHNSGNYLDWYLOKPGOSPOLLYLGSNRA 60

Db	1	DIWMTOSPLSLPVTGPSPASISCRSSQSLHNSGYNILDWYLRKPGSGPQLIYLGSNRA	60
Qy	61	SGVPDRFSSGGSGTDTFLKISRVEADVGVVYQWALQSLMCSFGGQTKLEIK	113
Db	61	SGVPDRFSSGGSGTDTFLKISRVEADVGVVYQWALQTPYTFGGQTKLEIK	112

RESULT '12
US-11-021-715-75
; Sequence 75, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-75

	Query Match	92.8%	Score 547.5;	DB 6;	Length 112;
	Best Local Similarity	94.7%;	Pred. No. 3.2e-42;		
	Matches 107;	Conservative 3;	Mismatches 2;	Indels 1;	Gaps 1;
Qy	1	DIWMTQSLPVTTPGEPASISCRSSQSLLHNSGYNLDWYLOKPGQSPOLLIIVLSNRA	60		
Db	1	DIWMTQSLPVTTPGEPASISCRSSQSLLHNSGYNLDWYLOKPGQSPOLLIIVLSNRA	60		
Qy	61	SGVPDRFSGSGSTDFTLKLSRVEADVGVVYCWQALQSLMCSFGQGTKEIK	113		
Db	61	SGVPDRFSGSGSTDFTLKLSRVEADVGVVYCWQALQSLMCSFGQGTKEIK	112		

RESULT 13
US-11-021-715-92
; Sequence 92, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-92

Query Match	92.8%	Score 547.5;	DB 6;	Length 112;
Best Local Similarity	92.9%	Pred. No. 3.2e-42;		

Search completed: April 25, 2007, 04:22:50
Job time : 41.8164 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 04:23:02 ; Search time 44 Seconds
(without alignments)
533.620 Million cell updates/sec

Title: US-10-665-383-40

Perfect score: 590

Sequence: 1 DIVMTQSPSLPVTGEPAS.....MQALQSLMCSFGQGTKEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 947558 seqs, 205760075 residues

Total number of hits satisfying chosen parameters: 947558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New.*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	113	7 US-11-109-181-30	Sequence 30, Appl
2	590	100.0	113	7 US-11-109-181-221	Sequence 221, Appl
3	590	100.0	113	7 US-11-109-181-255	Sequence 255, Appl
4	576.5	97.7	114	7 US-11-109-181-322	Sequence 322, Appl
5	554	93.9	114	7 US-11-428-895-19	Sequence 19, Appl
6	554	93.9	131	7 US-11-428-895-25	Sequence 25, Appl
7	550	93.2	111	7 US-11-433-924-268	Sequence 268, Appl
8	550	93.2	223	7 US-11-396-178-98	Sequence 98, Appl
9	550	93.2	223	7 US-11-396-178-156	Sequence 156, Appl
10	548	92.8	112	7 US-11-428-895-20	Sequence 20, Appl
11	547.5	92.6	112	7 US-11-211-917-104	Sequence 104, Appl
12	546.5	92.6	112	7 US-11-256-332-128	Sequence 128, Appl
13	546.5	92.6	112	7 US-11-369-641-4	Sequence 4, Appli
14	546.5	92.6	113	7 US-11-256-332-118	Sequence 118, Appl
15	546.5	92.6	113	7 US-11-311-939-639	Sequence 639, Appl
16	546.5	92.6	115	7 US-11-256-332-73	Sequence 73, Appl
17	546.5	92.6	115	7 US-11-256-332-81	Sequence 81, Appl
18	546.5	92.6	115	7 US-11-256-332-89	Sequence 89, Appl
19	546.5	92.6	115	7 US-11-256-332-97	Sequence 97, Appl
20	546.5	92.6	134	7 US-11-303-478-8	Sequence 8, Appli
21	546.5	92.6	134	7 US-11-303-899-68	Sequence 68, Appl
22	544.5	92.5	112	7 US-11-511-164-8	Sequence 8, Appli
23	544.5	92.3	111	7 US-11-311-939-646	Sequence 646, Appl
24	544.5	92.3	112	7 US-11-239-308-16	Sequence 16, Appl
25	544.5	92.3	112	7 US-11-211-917-103	Sequence 103, Appl

ALIGNMENTS

RESULT 1

US-11-109-181-30
; Sequence 30, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Biyem
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/11/109,181
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US/10/041,860
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 113
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-181-30

Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 5e-48;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLIYIGSNRA 60

DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLIYIGSNRA 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEADGVYVYCMQALQSLMCSFGQGTKEIK 113

DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVYVYCMQALQSLMCSFGQGTKEIK 113

RESULT 2

US-11-109-181-221
; Sequence 221, Application US/11109181
; Publication No. US20060293506A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX 051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 221
LENGTH: 113
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-221

Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 5e-48;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSGTDFTLKISRVEADDGVYYCMAQLQSLMCSFGGQTKLEIK 113
Db 61 SGVPDRFSGSGTDFTLKISRVEADDGVYYCMAQLQSLMCSFGGQTKLEIK 113

RESULT 3
US-11-109-181-255
Sequence 255, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX 051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 255
LENGTH: 113
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-255

Query Match 100.0%; Score 590; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 5e-48;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSGTDFTLKISRVEADDGVYYCMAQLQSLMCSFGGQTKLEIK 113
Db 61 SGVPDRFSGSGTDFTLKISRVEADDGVYYCMAQLQSLMCSFGGQTKLEIK 113

RESULT 4
US-11-109-181-322
Sequence 322, Application US/11109181
Publication No. US20060293506A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX 051A
CURRENT APPLICATION NUMBER: US/11/109,181
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/10/041,860
PRIOR FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 322
LENGTH: 114
TYPE: PRT
ORGANISM: homo sapiens
US-11-109-181-322

Query Match 97.7%; Score 576.5; DB 7; Length 114;
Best Local Similarity 98.2%; Pred. No. 9.3e-47;
Matches 112; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSGTDFTLKISRVEADDGVYYCMAQLQSLMCSFGGQTKLEIK 113
Db 61 SGVPDRFSGSGTDFTLKISRVEADDGVYYCMAQLQSLMCSFGGQTKLEIK 114

RESULT 5
US-11-428-895-19
Sequence 19, Application US/11428895
Publication No. US20070003554A1
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
of Antibodies to Human Platelet Glycoprotein Ib Alpha
FILE REFERENCE: 011.00231
CURRENT APPLICATION NUMBER: US/11/428,895
CURRENT FILING DATE: 2006-07-06
PRIOR APPLICATION NUMBER: US/09/430,048
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/106,275
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-11-428-895-19

Query Match 93.9%; Score 554; DB 7; Length 114;
Best Local Similarity 93.8%; Pred. No. 1.2e-44;
Matches 106; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLSNRA 60

APPLICANT: JIA, Xiao-Chi
APPLICANT: GUDAS, Jean
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
TITLE OF INVENTION: BIND TO 16P2F10B PROTEINS
FILE REFERENCE: 511582006221
CURRENT APPLICATION NUMBER: US/11/396,178
CURRENT FILING DATE: 2006-03-31
PRIOR APPLICATION NUMBER: 10/291,241
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 10/005,480
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/667,588
PRIOR FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: 60/700,975
PRIOR FILING DATE: 2005-07-20
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 156
LENGTH: 223
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: 211
OTHER INFORMATION: Xaa = Any amino acid.
US-11-396-178-156

Query Match 93.2%; Score 550; DB 7; Length 223;
Best Local Similarity 93.8%; Pred. No. 5.8e-44;
Matches 106; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

QY 1 DIVMTQSLSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 8 DIVMTQSLSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 67
QY 61 SGVPRFSGSGGTDTFLKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113
DB 68 SGVPRFSGSGGTDTFLKISRVEADDGVVYCMQALQTI--TFQGTKEIK 118

RESULT 10

US-11-428-895-20
Sequence 20, Application US/11428895
Publication No. US20070003554A1
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L
TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions
TITLE OF INVENTION: of Antibodies to Human Platelet Glycoprotein Ib Alpha
FILE REFERENCE: 011.00231
CURRENT APPLICATION NUMBER: US/11/428,895
CURRENT FILING DATE: 2006-07-06
PRIOR APPLICATION NUMBER: US/09/430,048
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/106,275
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-11-428-895-20

Query Match 92.9%; Score 548; DB 7; Length 112;
Best Local Similarity 94.7%; Pred. No. 4.4e-44;
Matches 107; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 DIVMTQSLSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSLSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113

Db 61 SGVPRFSGSGGTDTFLKISRVEADDGVVYCMQALQTI--PTFGQGTKEIK 111

RESULT 11

US-11-211-917-104
Sequence 104, Application US/11211917
Publication No. US20060093600A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/11/211,917
CURRENT FILING DATE: 2005-08-25
PRIOR APPLICATION NUMBER: US/10/292,088
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 104
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-11-211-917-104

Query Match 92.8%; Score 547.5; DB 7; Length 112;
Best Local Similarity 94.7%; Pred. No. 4.8e-44;
Matches 107; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
QY 1 DIVMTQSLSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
DB 1 DIVMTQSLSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDGVVYCMQALQSLMCSFGQGTKEIK 113
DB 61 SGVPRFSGSGGTDTFLKISRVEADDGVVYCMQALQTI--PYTFQGTKEIK 112

RESULT 12

US-11-256-332-128
Sequence 128, Application US/11256332
Publication No. US20060228349A1
GENERAL INFORMATION:
APPLICANT: Acton, Paul
APPLICANT: An, Zhidong
APPLICANT: Bett, Andrew J.
APPLICANT: Breese, Robert
APPLICANT: Chen Dodson, Elizabeth
APPLICANT: Kinney, Gene
APPLICANT: Klein, William R.
APPLICANT: Kraft, Grant A.
APPLICANT: Lambert, Mary P.
APPLICANT: Liang, Xiaoping
APPLICANT: Pray, Todd R.
APPLICANT: Shughrue, Paul
APPLICANT: Strohl, William R.
APPLICANT: Wang, Fubao
TITLE OF INVENTION: ANTI-ADDL ANTIBODIES AND USES THEREOF
FILE REFERENCE: MRK0002US
CURRENT APPLICATION NUMBER: US/11/256,332
CURRENT FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: US 60/621,776
PRIOR FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US 60/652,538
PRIOR FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: US 60/695,528
PRIOR FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: US 60/695,526
PRIOR FILING DATE: 2005-06-30


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; NUMBER OF SEQ ID NOS: 322
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-256-332-128

Query Match          92.6%; Score 546.5; DB 7; Length 112;
Best Local Similarity 93.8%; Pred. No. 6e-44;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 112

RESULT 13
US-11-369-641-4
; Sequence 4, Application US/11369641
; Publication No. US20060258852A1
; GENERAL INFORMATION:
; APPLICANT: Lugovskoy, Alexey Alexandrovich et al.
; TITLE OF INVENTION: METHODS OF HUMANIZING IMMUNOGLOBULIN VARIABLE REGIONS
; TITLE OF INVENTION: THROUGH RATIONAL MODIFICATION OF COMPLEMENTARITY
; TITLE OF INVENTION: DETERMINING REGIONS
; FILE REFERENCE: BGN-A230
; CURRENT APPLICATION NUMBER: US/11/369,641
; CURRENT FILING DATE: 2006-03-06
; PRIOR APPLICATION NUMBER: 60/658,987
; PRIOR FILING DATE: 2005-03-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 112
; ORGANISM: Homo sapiens
US-11-369-641-4

Query Match          92.6%; Score 546.5; DB 7; Length 112;
Best Local Similarity 93.8%; Pred. No. 6e-44;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 112

RESULT 14
US-11-256-332-118
; Sequence 118, Application US/11256332
; Publication No. US20060228349A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Paul
; APPLICANT: An, Zhigang
; APPLICANT: Bett, Andrew J.
; APPLICANT: Breese, Robert
; APPLICANT: Chen Dodson, Elizabeth
; APPLICANT: Kinney, Gene
; APPLICANT: Klein, William R.
; APPLICANT: Kraft, Grant A.
; APPLICANT: Lambert, Mary P.
; APPLICANT: Liang, Xiaoping
; APPLICANT: Pray, Todd R.
; APPLICANT: Shughrue, Paul

; NUMBER OF SEQ ID NOS: 322
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-256-332-118

Query Match          92.6%; Score 546.5; DB 7; Length 113;
Best Local Similarity 93.8%; Pred. No. 6.1e-44;
Matches 106; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113
Db 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 112

RESULT 15
US-11-311-939-639
; Sequence 639, Application US/11311939
; Publication No. US20060246071A1
; GENERAL INFORMATION:
; APPLICANT: Green, Larry L.
; APPLICANT: Zhou, Qing
; APPLICANT: Keyt, Bruce A.
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Emery, Stephen
; APPLICANT: Blakey, David C.
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO ANGIOPOIETIN-2
; FILE REFERENCE: ABXAZ.002A
; CURRENT APPLICATION NUMBER: US/11/311,939
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: US 60/638,354
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/711,289
; PRIOR FILING DATE: 2005-08-25
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-311-939-639

Query Match          92.6%; Score 546.5; DB 7; Length 113;
Best Local Similarity 93.8%; Pred. No. 6.1e-44;
Matches 106; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHSGNYNLDWYLOKPGQSPQLLIYLGSNRA 60
QY 61 SGVPRFSGSGGTDTFLKISRVEADDVGVYCMQALQSLMCSFGQGTKEIK 113
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Db 61 SGVDRFSGSGTDFTLKISRVEADVGVYCMQALOTPI-TFGQTRLEIK 112

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